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On protein - Protein search, using sw model		
Run on:	July 8, 2003, 12:12:22 ; Search time 70 Seconds (without alignments) 725.264 Million cell updates/sec	
Title:	US-09-901-910-2	
Perfect score:	2115	
Sequence:	1 MSSRIARALALVVTLLHTR..... ANEAFFPYRLFNDIHKFRD 381	
Scoring table:	BLOSUM62	
Gapext:	0.5	
Searched:	908470 seqs, 133250620 residues	
Total number of hits satisfying chosen parameters:	908470	
Minimum DB seq length:	0	
Maximum DB seq length:	200000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
	Listing first 45 summaries	
Database :		
	A_Genesed_101002:*	
1:	/SIDS2/geodata/geneseq/geneseq/geneseqp-emb1/AA1980.DAT:*	
2:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1981.DAT:*	
3:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1982.DAT:*	
4:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1983.DAT:*	
5:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1984.DAT:*	
6:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1985.DAT:*	
7:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1986.DAT:*	
8:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1987.DAT:*	
9:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1988.DAT:*	
10:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1989.DAT:*	
11:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1990.DAT:*	
12:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1991.DAT:*	
13:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1992.DAT:*	
14:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1993.DAT:*	
15:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1994.DAT:*	
16:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1995.DAT:*	
17:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1996.DAT:*	
18:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1997.DAT:*	
19:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1998.DAT:*	
20:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA1999.DAT:*	
21:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA2000.DAT:*	
22:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA2001.DAT:*	
23:	/SIDS2/geodata/geneseq/geneseqp-emb1/AA2002.DAT:*	
	PRED. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
	SUMMARIES	
Result No.	Score	
	Query Match Length DB ID	
	Description	
1	2115 100.0 381 18 AAW35957	Human monocyte mat
2	2115 100.0 381 22 AAB90773	Human shear stress
3	2115 100.0 381 23 AAU79761	Human Cyr61 prote
4	2115 100.0 381 23 AAE18107	Human connective t
5	2115 100.0 381 23 ABB05438	Human Cyr61 prote
6	2115 100.0 455 21 AAB43087	Human cancer assoc
7	2106 99.6 381 18 AAW35730	Human cysteine-ric
8	2106 99.6 381 22 AAE05921	Human cysteine-ric
9	1980.5 93.6 374 23 ABB09302	HCGF CNN family pr
10	1980.5 93.6 375 17 AAR90919	Connective tissue

ALIGNMENTS	
RESULT 1	
ID	AAW35957 standard; Protein; 381 AA.
XX	
AC	AAW35957;
XX	
DT	05-MAR-1998 (first entry)
XX	
DE	Human monocyte mature differentiation factor.
XX	
KW	Human; monocyte; mature; differentiation factor; MDDF; macrophage; cancer; immune activator; tissue culture; infectious disease.
XX	
OS	Homo sapiens.
XX	
PN	JP09234079-A.
XX	
PD	09-SEP-1997.
XX	
PF	04-MAR-1996; 96JP-0075236.
PR	04-MAR-1996; 96JP-0075236.
XX	
PA	(TOYOM) TOYOB0 KK.
XX	
DR	WPI: 1997-497320/46.
XX	
DR	N-PSDB; AAF97142.
PT	A monocyte mature differentiation factor - useful for the long term
PT	tissue culture of macrophage(s)
XX	
PS	Claim 9; Page 12-13; 22PP; Japanese.
XX	

CC The present sequence represents a monocyte mature differentiation factor (MMDF) which maintains the life of macrophages for long periods in liquid culture. MMDF can be used as an anti-cancer agent, an immune activator and to treat infectious diseases.

CC Sequence 381 AA;

Query Match 100.0%; Score 2115; DB 18; Length 381; Best Local Similarity 100.0%; Pred. No. 5.1e-154; Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSSRIRALARALVVTIHLHTRIALSTCPAACHCPLAEAKPCKAPGVLVRDGGCCVKVCAKQL 60

Db 61 NEDCSKTQPCDHTKGLECNFGASSATALKGICRAOSEGRCEYNSRYIYONGESFOPNCKHQ 120

Db 61 NEDCSKTQPCDHTKGLECNFGASSATALKGICRAOSEGRCEYNSRYIYONGESFOPNCKHQ 120

Db 121 CTCIDGAVGCIPLCPOELSLPNLGPNCNPRLVKVNGQCCEWMEDDSIKDPMDQDGIG 180

Db 121 CTCIDGAVGCIPLCPOELSLPNLGPNCNPRLVKVNGQCCEWMEDDSIKDPMDQDGIG 180

Db 181 KELGDAEVELTRNNELAVGKGSSLKLRLPVFGMEPRLYNPIQGOKCIVQTWSQCS 240

Db 181 KELGDAEVELTRNNELAVGKGSSLKLRLPVFGMEPRLYNPIQGOKCIVQTWSQCS 240

Db 241 KTCGGIISTRVTNDNPECRLVKETRICEVRPGQPVYSSLLKGKKSITKSKPSPEVRTY 300

Db 241 KTCGGIISTRVTNDNPECRLVKETRICEVRPGQPVYSSLLKGKKSITKSKPSPEVRTY 300

Db 301 AGCLSVKKYRKYCGSCVGDRCCTPQLTRVKMRFRCDEGETFSKNVMMIQSCKNYNCP 360

Db 301 AGCLSVKKYRKYCGSCVGDRCCTPQLTRVKMRFRCDEGETFSKNVMMIQSCKNYNCP 360

Db 361 HANEAAPFPYRLFNDIHKFRD 381

PT useful in diagnosis and treatment of vascular disease caused by arteriosclerosis -
PT
CC
CC
CC
XX
PS
XX
The present invention provides the protein and coding sequences of a number of human shear stress response proteins. These are useful in the diagnosis, treatment and screening of vascular diseases caused by arteriosclerosis, including heart failure, post-PTCA restenosis and hypertension.

CC Sequence 381 AA;

Query Match 100.0%; Score 2115; DB 22; Length 381; Best Local Similarity 100.0%; Pred. No. 5.1e-154; Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSSRIRALARALVVTIHLHTRIALSTCPAACHCPLAEAKPCKAPGVLVRDGGCCVKVCAKQL 60

Db 61 NEDCSKTQPCDHTKGLECNFGASSATALKGICRAOSEGRCEYNSRYIYONGESFOPNCKHQ 120

Db 61 NEDCSKTQPCDHTKGLECNFGASSATALKGICRAOSEGRCEYNSRYIYONGESFOPNCKHQ 120

Db 121 CTCIDGAVGCIPLCPOELSLPNLGPNCNPRLVKVNGQCCEWMEDDSIKDPMDQDGIG 180

Db 121 CTCIDGAVGCIPLCPOELSLPNLGPNCNPRLVKVNGQCCEWMEDDSIKDPMDQDGIG 180

Db 181 KELGDAEVELTRNNELAVGKGSSLKLRLPVFGMEPRLYNPIQGOKCIVQTWSQCS 240

Db 181 KELGDAEVELTRNNELAVGKGSSLKLRLPVFGMEPRLYNPIQGOKCIVQTWSQCS 240

Db 241 KTCGGIISTRVTNDNPECRLVKETRICEVRPGQPVYSSLLKGKKSITKSKPSPEVRTY 300

Db 241 KTCGGIISTRVTNDNPECRLVKETRICEVRPGQPVYSSLLKGKKSITKSKPSPEVRTY 300

Db 301 AGCLSVKKYRKYCGSCVGDRCCTPQLTRVKMRFRCDEGETFSKNVMMIQSCKNYNCP 360

Db 301 AGCLSVKKYRKYCGSCVGDRCCTPQLTRVKMRFRCDEGETFSKNVMMIQSCKNYNCP 360

Db 361 HANEAAPFPYRLFNDIHKFRD 381

KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
 KW vasotrophic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ refection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening.
 OS Homo sapiens.
 XX
 PN WO20055350-A1.
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05882.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PT Rosen CA, Ruben SM;
 DR WPI; 2000-587533/55.
 DR N-PSDB; AAC78196.
 XX
 Novel isolated nucleic acids comprising sequences encoding peptides
 PT used for treating or diagnosing e.g. cancer -
 XX
 PS Claim 11; Page 2116-2118; 2352pp; English.
 XX
 AAC77607 to AAC78448 encode the human cancer associated proteins given
 CC in ARB43398 to ARB4239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; proliferative; vulnerary; immunomodulator;
 CC antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
 CC antiinflammatory; antithyroid; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC nootropic; vasotrophic; antipsoriatic and antiangiogenic. The
 CC polyurelectides and polyptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies/
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC7457 and ARB44240 represent sequences used in the exemplification of
 CC the present invention.
 XX
 Sequence 455 AA;
 SQ Query Match 100 %; Score 2115; DB 21; Length 455;
 Best Local Similarity 100 %; Pred. No. 6.3e-154;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSSRIRALARALWVTLHLTRIALSTCPACHPLEPKCARPGVLVRDGGCCCKYQAKL 60
 Db 75 MSRRIRALARALWVTLHLTRIALSTCPACHPLEPKCARPGVLVRDGGCCCKYQAKL 134
 Db 61 NEDCSKTPQCDTUGKLGECNGASASTALKIGCRAQSIGRCPCEYNSRITQNGESFQPNCHQ 120
 Qy 135 NEDCSKTPQCPHTKGLEGNGASASTALKIGCRAQSIGRCPCEYNSRITQNGESFQPNCHQ 194
 Qy 121 CTCIDGAVGCIPCPBLSLPLMGLCNPRLKVTGCGCEEWCGCDESKIDPMEDDGLG 180
 Db 195 CTCIDGAWGCIPCPBLSLPLMGLCNPRLKVTGCGCEEWCGCDESKIDPMEDDGLG 254
 Qy 181 KLGFDASEVELTRNNEELIAGKGSSLRPLPVFGMPRPLYNPLQOKCIWOTTSHQS 240
 Db 255 KLGFDASEVELTRNNEELIAGKGSSLRPLPVFGMPRILYNPLQOKCIVOTTSHQS 314

RESULT 7
 ID AAW35730 standard; Protein; 381 AA.
 AC AAW35730;
 XX
 PR 27-MAR-1998 (first entry)
 XX
 DE Human cysteine rich protein 61 (Cyr61).
 XX
 DR Cysteine rich protein 61; Cyr61; human;
 KW extracellular matrix signalling molecule; cell adhesion;
 KW cell migration; cell proliferation; angiogenesis; chondrogenesis;
 KW oncogenesis; haemostasis; wound healing; organ regeneration.
 XX
 OS Homo sapiens.
 XX
 PN WO9733995-A2.
 XX
 PR 18-SEP-1997.
 XX
 PT 14-MAR-1997; 97WO-US04193.
 XX
 DR WPI; 1997-470875/43.
 XX
 PR N-PSDB; AAC794699.
 XX
 PT Isolated and purified cysteine rich protein 61, Cyr61 - useful to
 PT modulate e.g. haemostasis, induce wound healing, promote organ
 PT regeneration etc.
 XX
 PI Lau LF;
 XX
 PR Claim 2; Page 112-113; 133pp; English.
 XX
 CC This protein sequence comprises human cysteine rich protein 61
 CC (Cyr61), an extracellular matrix signalling molecule. Its amino
 acid sequence was deduced from a human placental cDNA clone (see
 CC ARB4699). Cyr61 polypeptides can be expressed in transformed or
 CC transfected host cells. Cyr61 can be used to modulate
 CC haemostasis, induce wound healing in a tissue, promote organ
 CC regeneration, improve tissue grafting or promote bone or prothesis
 CC implantation (claimed). It can also be used to screen for a
 CC modulator of angiogenesis, chondrogenesis, oncogenesis, cell
 CC adhesion, cell migration, cell proliferation, expand a population
 CC of undifferentiated haematopoietic stem cells in culture and to
 CC screen for a mitogen (claimed). Ex vivo methods for using
 CC mammalian extracellular matrix signalling molecules to prepare
 CC blood products are also provided.
 XX
 SQ Sequence 381 AA;

Query Match 99.6%; Score 2106; DB 18; Length 381;
 Best Local Similarity 99.5%; Pred. No. 2.5e-153;
 Matches 379; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OS	Unidentified.	AC	AARR0919;
XX	US2002049304-A1.	PN	25-JUN-1996 (first entry)
XX	25-APR-2002.	DT	
PD		DE	Connective tissue growth factor-2.
XX		XX	
PR	14-MAY-2001; 2001US-0853625.	KW	CTGF-2; connective tissue growth factor-2; secreted protein;
PR	06-JUN-1995; 95US-0468947.	KW	cartilaginous growth; skeletal; embryo; cell growth; morphogenesis;
PR	01-APR-1998; 98US-0053587.	KW	insulin-like growth factor; fibroblast growth factor; Cry61.
XX		XX	
PA	(HAST/) HASTINGS G A.	OS	Homo sapiens.
PA	(ADAM/) ADAMS M D.	XX	
PT	Hastings GA, Adams MD;	FH	Key
PT	XX	FT	Location/Qualifiers
PT	WPI; 2002-382150/41.	FT	1..24
PS	PT	FT	/label= signal_peptide
PS	Disclosure; Fig 2A-D; 33pp; English.	FT	25..375
XX		FT	/label= mature_protein
XX		PN	
XX	Novel isolated polynucleotide sequence encoding a human small CCN-like	XX	W09601896-A.
PT	growth factor, useful for treating muscle wasting disease, and	PD	25-JAN-1996.
PT	osteoporosis -	XX	
XX		PF	12-JUL-1994; 94WO-US07736.
XX		PR	12-JUL-1994; 94WO-US07736.
CC	The present invention describes human small CCN-like growth factor	XX	
CC	(SCGF). SCGF has pulmonary and osteopathic activities, and can be used	PA	(HUMA-) HUMAN GENOME SCI INC.
CC	in gene therapy. The SCGF Polypeptides and polynucleotides can be used	XX	
CC	for treating muscle wasting diseases, and osteoporosis, and to stimulate	PT	Adams MD, Li H;
CC	wound healing and tissue regeneration, to promote angiogenesis and to	XX	
CC	stimulate proliferation of vascular smooth muscle and endothelial cell	DR	WPI; 1996-097626/10.
CC	production. The present sequence represents a CNN family protein which	DR	N-PSDB; AAT12653.
CC	is given in comparison with the human SCGF in the exemplification of the	XX	
CC	present invention.	PT	
XX	sequence 374 AA;	PT	Connective tissue growth factor-2 and DNA encoding it - useful to
XX		PT	enhance the repair of connective and support tissue, and to enhance
XX		PT	wound healing
PS	Claim 1; Fig 1A-C; 46pp; English.	XX	
PS		CC	Connective tissue growth factor-2 (CTGF-2) is encoded by a cDNA
PS		CC	(AAT12653) isolated from a human foetal lung cDNA library. The GTGF
PS		CC	polypeptides are structurally and functionally related to a family
PS		CC	of growth factors which include IGF (insulin-like growth factor),
PS		CC	PDGF (platelet-derived growth factor), and PGF (fibroblast growth
PS		CC	factor). CTGF-2 exhibits 89 percent identity and 93 percent similarity
PS		CC	to Cry61. Cry61 is a growth factor-inducible immediate early gene
PS		CC	initially identified in serum-stimulated mouse fibroblasts. It encodes
PS		CC	a member of an emerging family of secreted proteins which are also a
PS		CC	group of cysteine-rich proteins. This group of GRS are important for
PS		CC	normal growth, differentiation, morphogenesis of the cartilaginous
PS		CC	skeleton of an embryo and cell growth.
PS	Sequence 375 AA;	XX	
Query Match	93.6%; Score 1980.5; DB 17; Length 375;	OS	
Matches 360; Conservative 1; Mismatches 12; Indels 1; Gaps 1;			
QY	1 MSSRARALAVVLTLLHLTRALSTCPAACHCPEAKPCAPGVLVRDGCCCKYCAKQL 60	QY	1 MSSRARALAVVLTLLHLTRALSTCPAACHCPEAKPCAPGVLVRDGCCCKYCAKQL 60
Db	1 MSSRARALAVVLTLLHLTRALSTCPAACHCPEAKPCAPGVLVRDGCCCKYCAKQL 60	Db	1 MSSRARALAVVLTLLHLTRALSTCPAACHCPEAKPCAPGVLVRDGCCCKYCAKQL 60
QY	241 SKTCGTG1STRYVINDNPCCR1VKE1TICEEVRCGQPVYSSLKKKGKCSKTKSPPVRF 299	QY	241 SKTCGTG1STRYVINDNPCCR1VKE1TICEEVRCGQPVYSSLKKKGKCSKTKSPPVRF 300
Db	241 SKTCGTG1STRYVINDNPCCR1VKE1TICEEVRCGQPVYSSLKKKGKCSKTKSPPVRF 300	Db	241 SKTCGTG1STRYVINDNPCCR1VKE1TICEEVRCGQPVYSSLKKKGKCSKTKSPPVRF 300
QY	300 YAGCLSYKRYPKYCSCVDGRCTPQLTRTVKMRFRCEDGEFTSKYTM1Q5CKCN1C 359	QY	301 YAGCLSYKRYPKYCSCVDGRCTPQLTRTVKMRFRCEDGEFTSKYTM1Q5CKCN1C 360
Db	301 YAGCLSYKRYPKYCSCVDGRCTPQLTRTVKMRFRCEDGEFTSKYTM1Q5CKCN1C 359	Db	301 YAGCLSYKRYPKYCSCVDGRCTPQLTRTVKMRFRCEDGEFTSKYTM1Q5CKCN1C 360
QY	360 PHANEAAKPYRF 373	QY	360 PHANEAAKPYRF 373
Db	360 PHANEAAKPYRF 373	Db	360 PHANEAAKPYRF 373
Db	361 PHANEAAKPYRF 374	Db	361 PHANEAAKPYRF 374
RESULT 10			
AAR90919			
ID	AAR90919 standard; protein: 375 AA.	QY	180 GKG1GFDASEVELTRNNELIAVGKSSKLRLPVFGMPEIRLYNPLQGOKCIVOTWSQC 239
XX		QY	181 GKG1GFDASEVELTRNNELIAVGKSSKLRLPVFGMPEIRLYNPLQGOKCIVOTWSQC 240

CC support tissue and can therefore treat skin disorders e.g., acne, aging,
 CC UV damage or burns. CTGF-2 can be used to promote the attachment,
 CC fixation and stabilization of tissue implants inserted during
 CC reconstructive surgery, and can be used to enhance the healing of
 CC external wounds. It can be used in the treatment of injured or depleted
 CC bone as it promotes the growth of connective tissue, bone and cementum
 CC and stimulates protein and collagen synthesis.

QY 240 SKTCGTGISTRVNDNPCEPLVKETRICEVPRCQPVYSSLKKKKCSKTKSPEPYRFT 299
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC
 241 SKTCGTGISTRVNDNPCEPLVKETRICEVPRCQPVYSSLKKKKCSKTKSPEPYRFT 300
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC
 QY 300 YAGCLSVKVKYRKPKVCGSCVDGRCCTPQLTRTVKMRFCRCDGETFSKNYMMIOSCKCNINC 359
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC
 Db 301 YAGCLSVKVKYRKPKVCGSCVDGRCCTPQLTRTVKMRFCRCDGETFSKNYMMIOSCKCNINC 360
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 SQ
 QY 360 PHANEAAFPFYRLF 373
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 PHANEAAFPFYRLF 374
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query Match 93.6%; Score 1980.5; DB 20; Length 375;
 Best Local Similarity 96.3%; Pred. No. 1e-143; Mismatches 1; Gaps 1;
 Matches 360; Conservative 1; Indels 1; Gaps 1;

QY 1 MSSRIARALAVVTLHLTRALSTCPAACHCPLAEAPKCAPGVGLVRDGCGCCVKCAKOL 60
 ||||| | ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MSSRIVRELAVVTLHLTRVGLSTCPADCHCPLAEAPKCAPGVGLVRDGCGCCVKCAKOL 60
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 NEDCSKTTPCDHURKGLENGFGASSTALKIGCRASEGPGCENSRIVONGESRQPNCHQ 120
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 NEDCKTTOPCDHTRGLECNFGASSTALKIGCRASEGPGCENSRIVONGESRQPNCHQ 120
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DE Human CTGF-2.
 XX
 KW Connective tissue growth factor-2; CTGF-2; wound healing; bone disorder;
 KW skin disorder; acne; burn; UV damage; stabilisation; tissue implant.
 XX
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 Peptide 1..24
 FT /label= Signal_Peptide
 Protein 25..375
 FT Misc-difference 268
 FT /note= "Cys encoded by ICT"
 XX
 US5945300-A.
 PN 121 CTCIDGAVG-CIPLCPOELSLPNUGCPAPRLVAVTGOCCEEWVCDEDSIKDMEDQCLL 179
 XX
 PR 121.CTCIDGAVG-CIPLCPOELSLPNUGCPAPRLVAVTGOCCEEWVCDEDSIKDMEDQCLL 179
 PR 31-AUG-1999.
 PR 95US-0459101.
 PR 02-JUN-1995;
 PR 95US-0459101.
 PR 12-JUL-1994;
 PR 94WO-US07736.
 PA (ADAM/) ADAMS M D.
 PA (LHH/) LI H.
 PI Adams MD, LI H;
 PI
 XX
 DR WPI: 1999-508171/42.
 DR N-PSDB; AAZ11720.
 XX
 PT Polynucleotides encoding growth factor polypeptides useful for
 enhancing the repair of connective tissue and support tissue
 PS Claim 1; 20pp; English.
 XX
 This sequence represents human connective tissue growth factor-2
 (CTGF-2). CTGF-2 cDNA was isolated from a cDNA library derived from
 CC human fetal lung. In one instance, the cDNA was cloned into a
 CC baculovirus expression vector, having first been amplified and modified
 CC via PCR using primers AAZ11721 and AAZ11722. In another instance, the
 CC cDNA was cloned into a COS cell expression vector, with prior
 CC amplification and modification using PCR primers AAZ11723 and AAZ11724.
 CC CTGF-2 is structurally and functionally related to a family of growth
 factors which include IGF (insulin-like growth factor), PDGF
 CC (platelet-derived growth factor) and FGF (fibroblast growth factor). This
 emerging family of cysteine-rich secreted proteins are important for
 CC normal growth, differentiation, morphogenesis of the cartilaginous
 CC skeleton of an embryo and cell growth. Their functions also include wound
 CC healing, tissue repair, implant fixation and stimulating increased bone
 mass. CTGF-2 may be used to enhance the repair of connective tissue and
 CC

CC support tissue and can therefore treat skin disorders e.g., acne, aging,
 CC UV damage or burns. CTGF-2 can be used to promote the attachment,
 CC fixation and stabilization of tissue implants inserted during
 CC reconstructive surgery, and can be used to enhance the healing of
 CC external wounds. It can be used in the treatment of injured or depleted
 CC bone as it promotes the growth of connective tissue, bone and cementum
 CC and stimulates protein and collagen synthesis.

QY 240 SKTCGTGISTRVNDNPCEPLVKETRICEVPRCQPVYSSLKKKKCSKTKSPEPYRFT 299
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC
 241 SKTCGTGISTRVNDNPCEPLVKETRICEVPRCQPVYSSLKKKKCSKTKSPEPYRFT 300
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC
 QY 300 YAGCLSVKVKYRKPKVCGSCVDGRCCTPQLTRTVKMRFCRCDGETFSKNYMMIOSCKCNINC 359
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 CC
 Db 301 YAGCLSVKVKYRKPKVCGSCVDGRCCTPQLTRTVKMRFCRCDGETFSKNYMMIOSCKCNINC 360
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 SQ
 Sequence 375 AA:

Query Match 93.6%; Score 1980.5; DB 20; Length 375;
 Best Local Similarity 96.3%; Pred. No. 1e-143; Mismatches 1; Gaps 1;
 Matches 360; Conservative 1; Indels 1; Gaps 1;

QY 1 MSSRIARALAVVTLHLTRALSTCPAACHCPLAEAPKCAPGVGLVRDGCGCCVKCAKOL 60
 ||||| | ||||| ||||| ||||| : ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MSSRIVRELAVVTLHLTRVGLSTCPADCHCPLAEAPKCAPGVGLVRDGCGCCVKCAKOL 60
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 180 GKEIGFDASEVELTRNNEILAVRGSSIKRLPVFGMERILYMPNPLQGOKCIVOTTSHQC 239
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 GKEIGFDASEVELTRNNEILAVRGSSIKRLPVFGMERILYMPNPLQGOKCIVOTTSHQC 240
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 121 CTCIDGAVG-CIPLCPOELSLPNUGCPAPRLVAVTGOCCEEWVCDEDSIKDMEDQCLL 180
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121.CTCIDGAVG-CIPLCPOELSLPNUGCPAPRLVAVTGOCCEEWVCDEDSIKDMEDQCLL 180
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 241 SKTCGTGISTRVNDNPCEPLVKETRICEVPRCQPVYSSLKKKKCSKTKSPEPYRFT 299
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 SKTCGTGISTRVNDNPCEPLVKETRICEVPRCQPVYSSLKKKKCSKTKSPEPYRFT 300
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 300 YAGCLSVKVKYRKPKVCGSCVDGRCCTPQLTRTVKMRFCRCDGETFSKNYMMIOSCKCNINC 359
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 YAGCLSVKVKYRKPKVCGSCVDGRCCTPQLTRTVKMRFCRCDGETFSKNYMMIOSCKCNINC 360
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 360 PHANEAAFPFYRLF 373
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 PHANEAAFPFYRLF 374
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Query Match 93.6%; Score 1980.5; DB 20; Length 375;
 Best Local Similarity 96.3%; Pred. No. 1e-143; Mismatches 1; Gaps 1;
 Matches 360; Conservative 1; Indels 1; Gaps 1;

QY 1 MSSRIARALAVVTLHLTRALSTCPAACHCPLAEAPKCAPGVGLVRDGCGCCVKCAKOL 60
 ||||| | ||||| ||||| ||||| : ||||| ||||| ||||| ||||| |||||
 Db 1 MSSRIVRELAVVTLHLTRVGLSTCPADCHCPLAEAPKCAPGVGLVRDGCGCCVKCAKOL 60
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DE Human alternative connective tissue growth factor-2 (CTGF-2).
 XX
 KW Human; angiogenesis; connective tissue growth factor-2; CTGF-2; tumour;
 KW ischaemia; restenosis; tissue repair; wound healing; congenital defect;
 KW cardiovascular disease; atherosclerosis; heart failure; angina; trauma;
 KW burns; osteoporosis; periodontal disease; liver failure; tranquilizer;
 KW vulnerability; cosmetic plastic surgery; vasotropics; hepatotropic; ulcer;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 WO200204480-A2.
 XX
 PD 17-JAN-2002.
 XX
 PR 11-JUL-2001; 2001WO-US21799.
 XX
 PR 11-JUL-2000; 2000US-217402P.
 PR 18-MAY-2001; 2001US-291642P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (TRGE-) TRANSGENE SA.

PI	Li H, Adams MD, Calenda V, Ratauccioli V;	XX	DT	18-JAN-1993 (first entry)
DR	WPI: 2002-171698/22.	XX	DE	Beta-1G-M1.
DR	N-PSDB; AAD29099.	XX	KW	Transforming growth factor beta; induced; CEF-10; v-src; chicken;
PT	Stimulating angiogenesis in a mammal preferably human having ischemia or restenosis or is treated for limb revascularization, by administering connective tissue growth factor-2 polypeptide or polyucleotide	XX	XX	embryo; fibroblasts; TGF-beta.
PT	or restenosis or is treated for limb revascularization, by administering connective tissue growth factor-2 polypeptide or polyucleotide	XX	OS	Mus musculus.
PS	Disclosure: Fig 11; 131pp; English.	XX	PN	EP495674 A.
XX	The present invention relates to a method for stimulating angiogenesis in a mammal. The method comprises administering a polyucleotide encoding connective tissue growth factor-2 (CTGF-2) or an active fragment or its derivative. The method is useful for stimulating angiogenesis in a mammal preferably human having ischaemia or restenosis or is treated for limb revascularisation which is leg or arm. The invention is useful for inhibiting tumour growth, where angiogenesis is utilised for enhancing the repair of connective and support tissue, promoting the attachment, fixation and stabilisation of tissue implants and enhancing wound healing, hence is useful for treating cardiovascular disease e.g., atherosclerosis, reperfusion injury such as heart failure, angina, ischaemia, and is also used to differentiate, proliferate and attract cells leading to regeneration of tissues which is utilised to repair, replace or protect tissue damaged by congenital defects, trauma (burns, ulcer, etc), age, disease (e.g. osteoporosis, periodontal disease, liver failure), surgery including cosmetic plastic surgery. The present sequence is human alternative CTGF-2. CTGF-2 gene is useful in gene therapy.	XX	PA (BRIM) BRISTOL-MYERS SQUIBB CO.	
XX	sequence 375 AA;	XX	PP	17-JAN-1992; 92EP-0300429.
Query Match	93.6%; Score 1980.5; DB 23; Length 375;	XX	PR	18-JAN-1991; 91US-0642991.
Best Local Similarity	96.3%; Pred. No. 1e-143;	XX	PR	10-JAN-1992; 92US-0816270.
Matches	360; Conservative 1; Mismatches 12; Indels 1; Gaps 1;	XX	PA	BRUNNER AM, CHINN J, NEUBAUER MG, PURCHIO AF;
QY	1 MSSRIARALALVYTILHULTRALSTCPAACHCPLAEAPKCAPGPVGLVRDGCCKVCAKQL 60	XX	PT	WPI; 1992-243108/30.
Db	1 MSSRIVRVLALAVVTLHLTRVGLSTCPADCHCPLAEAPKCAPGPVGLVRDGCCKVCAKQL 60	XX	DR	N-PSDB; AAD26421.
QY	61 NEDCSKIQOPCDHTKGLECNFGASSTALKIGICRAQSEGRCPEYNSRTYONGESTQPNCKHQ 120	XX	PS	Claim 2; Fig 1; 35pp; English.
Db	61 NEDCRKIQOPCDHTKGLECNFGASSTALKIGICRAQSEGRCPEYNSRTYONGESTQPNCKHQ 120	XX	CC	The protein sequence was deduced from the DNA sequence obt'd. by screening a cDNA library made from AKR-2B mouse cells induced with TGF-beta and cyclohexamide with two probes from untreated AKR-2B mRNA and AKR-2B mRNA from cells treated with cyclohexamide and TGF-beta. The proteins encoded by hybridizing colonies (beta-IG-M1 and beta-IG-M2) contain 38 Cys residues and are induced by TGF-beta. Beta-IG-M1 displays 80 percent homology to the CEF-10 protein induced by v-src in chicken embryo fibroblasts and is identical to the protein encoded by cys61, an immediate early response gene induced in quiescent BALB 3T3 cells by serum treatment. Residues 49-56 of beta-IG-M1 conform to the GGCX _n X motif reported in the amino half of insulin-like growth factor (IGF) binding proteins. The C-terminal Cys rich region of beta-IG-M1, -M2 and CEF-10 contain an amino acid sequence with strong homology to a motif found near the C-terminal of the malarial circumsporozoite (CS) protein, which is highly conserved among all species of malarial parasites sequenced to date (designated region II). This motif is also found in other proteins which have cell adhesive properties that mediate cell-cell and cell-extracellular matrix interactions, such as prooprin, thrombospondin, and TRAP. The proteins encoded by TGF-beta induced genes are likely to be involved in mediation of the biological effects of TGF-beta relating to cell growth and differentiation. See also AAR25566.
QY	121 CTCIDGAVG-CIPLCPQELSPLNPGCPNPLVKTGQCEEWVQEDDSIKDPMDQDGIL 179	XX	CC	CC
Db	121 CTCIDGAVG-CIPLCPQELSPLNPGCPNPLVKTGQCEEWVQEDDSIKDPMDQDGIL 179	XX	CC	CC
QY	121 CTCIDGAVG-CIPLCPQELSPLNPGCPNPLVKTGQCEEWVQEDDSIKDPMDQDGIL 179	XX	CC	CC
Db	121 CTCIDGAVG-CIPLCPQELSPLNPGCPNPLVKTGQCEEWVQEDDSIKDPMDQDGIL 179	XX	CC	CC
QY	180 GKELGDAESEVELTRNNELIAVGKSSLKRLPFGMERICLMPNLQGQKCIQVTTWSOC 239	XX	CC	CC
Db	180 GKELGDAESEVELTRNNELIAVGKSSLKRLPFGMERICLMPNLQGQKCIQVTTWSOC 239	XX	CC	CC
QY	181 GKGLGDAESEVELTRNNELIAVGKSSLKRLPFGMERICLMPNLQGQKCIQVTTWSOC 240	XX	CC	CC
Db	181 GKGLGDAESEVELTRNNELIAVGKSSLKRLPFGMERICLMPNLQGQKCIQVTTWSOC 240	XX	CC	CC
QY	240 SKTCGTGIGSTRVINDNPCLRYKETRICEVPRPGQPVVSSLKKGKCKSCTKKSPEPVRT 299	XX	CC	CC
Db	241 SKTCGTGIGSTRVINDNPCLRYKETRICEVPRPGQPVVSSLKKGKCKSCTKKSPEPVRT 300	XX	CC	CC
QY	300 YAGCLSTKVKYRPKYCGSCVDGRCTPOLTTRVUMFRERDEGEFSKNTMVIQSKCNCNYC 359	XX	CC	CC
Db	301 YAGCLSTKVKYRPKYCGSCVDGRCTPOLTTRVUMFRERDEGEFSKNTMVIQSKCNCNYC 360	XX	CC	CC
QY	360 PHANEAAFPYRLF 373	XX	CC	CC
Db	361 PHANEAAFPYRLF 374	XX	CC	CC
RESULT 13		XX	CC	CC
AAR25565		XX	CC	CC
ID	standard; Protein: 379 AA.	XX	CC	CC
AC	AAR25565;	XX	CC	CC

Db	179 -LGDLSEVELTRNNELIAGKSSLRKLPVPGCPRLPENPLAHGOKIVOTWSQ	CC
Qy	239 CSKTCGTGISTRVTNDNPECRLVKTRICRVEPRCCQPVYSSIKKKCSKTKSKSPEPVRF	CC
Db	237 CSKSCGTGISTRVTNDNPECRLVKTRICRVEPRCCQPVYSSIKKKCSKTKSKSPEPVRF	CC
Qy	299 TYAGCLSVKKYRPKKGSCUDRCRCCPQLRTVKMRFRCEDGEMFSKNVMMIQSCRNIN	CC
Db	297 TYAGCSSVKKYRPKKGSCUDRCRCCPQLRTVKMRFRCEDGEMFSKNVMMIQSCRNIN	CC
Qy	359 CPHANEAAPFPYRLENDIKFRD 381	CC
Db	357 CPHNEASFLYSLENDIKFRD 379	CC
RESULT 14		SQ
ID AAE05920		Sequence 379 AA:
XX AAE05920 standard; Protein: 379 AA.		
AC AAE05920;		
XX DT 24-SEP-2001 (first entry)		
DE XX		
Mouse cysteine-rich protein (Cyr61).		
KW Cysteine-rich protein; Cyr61; extracellular matrix signalling molecule; fibroblast secreted protein; Fisp12; connective tissue growth factor; KW angiogenesis; wound healing; integrin receptor; atherosclerosis; tumour; heart disease; fibrosis; gene therapy; mouse.		
OS XX		
Mus musculus.		
PH XX		
Key Location/Qualifiers		
Region 164..216		
/note= "Cysteine free region"		
FT Domain 224..240		
FT /note= "Domain III"		
XX PN WO200155210-A2.		
PD XX		
02-AUG-2001.		
XX PF 31-JAN-2001; 2001WO-US03267.		
PR 31-JAN-2000; 2000US-0495448.		
PR 15-MAY-2000; 2000US-0204364.		
PR 06-OCT-2000; 2000US-0238705.		
XX PA (MUNI-) MUNIN CORP.		
XX PI Lau LF, Yeung C, Greenspan JA;		
DR WPI-2001-465551/50.		
XX N_PDB: RADI1220.		
PS Example 1; Fig 1; 186pp; English.		
XX		
CC The invention relates to extracellular matrix (ECM) signalling molecules involved in cellular response to growth factors. More particularly the invention is directed to cysteine-rich protein (Cyr61), and Cyr61-related proteins such as fibroblast secreted protein (Fisp12) and connective tissue growth factor (CTGF) and nucleic acid molecules encoding such proteins. The polypeptides of the invention are members of cysteine-rich secreted protein family. Human CYR61 fragment is useful in methods for screening modulators of cell adhesion, cell migration, fibroblast cell proliferation, angiogenesis, wound healing and Cyr61-intein		
CC		
CC treatment of atherosclerosis, heart disease, tumor metastasis, fibrosis, tumour growth, disorders associated with inadequate angiogenesis; aberrant granulation tissue development; aberrant fibroblast growth and wounds. Polynucleotides of the invention are useful in gene therapy. The present sequence is mouse Cyr61 protein.		
CC		
CC		
CC receptor interaction. Modulator of Cyr61-intein		
CC interaction is used for the preparation of a medicament for the treatment of atherosclerosis, heart disease, tumor metastasis, fibrosis, tumour growth, disorders associated with inadequate angiogenesis; aberrant granulation tissue development; aberrant fibroblast growth and wounds. Polynucleotides of the invention are useful in gene therapy. The present sequence is mouse Cyr61 protein.		
Qy 1 MSSRIARALAVVTLHLTRALSTCPACRCPLEPKCPAEGVGLVPGCGCKVKCAKL 60	Qy	
Db 1 MSSSTFRHLAVVTLHLTRALSTCPACRCPLEPKCPAEGVGLVPGCGCKVKCAKL 60	Db	
Qy 61 NEDCSKTQPDCPDTKGLCNGFASSTAALKGICRAQESEPCENSRITQYONGESFQPNKHO 120	Qy	
Db 61 NEDCSKTQPDCPDTKGLCNGFASSTAALKGICRAQESEPCENSRITQYONGESFQPNKHO 120	Db	
Qy 121 CTCIDGAVGCTPLCPQELSPNLGCNPRLVKGQDCEEWYCDEDSTKDSLDDDL- 178	Qy	
Db 121 CTCIDGAVGCTPLCPQELSPNLGCNPRLVKGQDCEEWYCDEDSTKDSLDDDL- 178	Db	
Qy 181 KELGFDASEVELTRNNELIAVGKSSLRKLPFGMERILYPL- -OGOKCIQVOTWSQ 238	Qy	
Db 181 KELGFDASEVELTRNNELIAVGKSSLRKLPFGMERILYPL- -OGOKCIQVOTWSQ 238	Db	
Qy 179 - LGDLSEVELTRNNELIAGKSSLRKLPFGTEEVLFNLPHANGOKIVOTWSQ 236	Qy	
Db 179 - LGDLSEVELTRNNELIAGKSSLRKLPFGTEEVLFNLPHANGOKIVOTWSQ 236	Db	
Qy 239 CSKTCGTGISTRVTNDNPECRLVKTRICRVEPRCCQPVYSSIKKKCSKTKSKSPEPVRF 298	Qy	
Db 237 CSKSCGTGISTRVTNDNPECRLVKTRICRVEPRCCQPVYSSIKKKCSKTKSKSPEPVRF 298	Db	
Qy 299 TYAGCLSVKKYRPKKGSCUDRCRCCPQLRTVKMRFRCEDGEMFSKNVMMIQSCRNIN 356	Qy	
Db 297 TYAGCSSVKKYRPKKGSCUDRCRCCPQLRTVKMRFRCEDGEMFSKNVMMIQSCRNIN 356	Db	
Qy 359 CPHANEAAPFPYRLENDIKFRD 381	Qy	
Db 357 CPHNEASFLYSLENDIKFRD 379	Db	
Query Match 91.6%; Score 1938; DB 22; Length 379;	Query	
Best Local Similarity 91.4%; Pred. No. 1 8e-140; Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2; C	Match	
Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2; C	Matches	
Sequence 379 AA:	Sequence	
Qy 1 MSSRIARALAVVTLHLTRALSTCPACRCPLEPKCPAEGVGLVPGCGCKVKCAKL 60	Qy	
Db 1 MSSSTFRHLAVVTLHLTRALSTCPACRCPLEPKCPAEGVGLVPGCGCKVKCAKL 60	Db	
Qy 61 NEDCSKTQPDCPDTKGLCNGFASSTAALKGICRAQESEPCENSRITQYONGESFQPNKHO 120	Qy	
Db 61 NEDCSKTQPDCPDTKGLCNGFASSTAALKGICRAQESEPCENSRITQYONGESFQPNKHO 120	Db	
Qy 121 CTCIDGAVGCTPLCPQELSPNLGCNPRLVKGQDCEEWYCDEDSTKDSLDDDL- 178	Qy	
Db 121 CTCIDGAVGCTPLCPQELSPNLGCNPRLVKGQDCEEWYCDEDSTKDSLDDDL- 178	Db	
Qy 181 KELGFDASEVELTRNNELIAVGKSSLRKLPFGMERILYPL- -OGOKCIQVOTWSQ 238	Qy	
Db 181 KELGFDASEVELTRNNELIAVGKSSLRKLPFGMERILYPL- -OGOKCIQVOTWSQ 238	Db	
Qy 179 - LGDLSEVELTRNNELIAGKSSLRKLPFGTEEVLFNLPHANGOKIVOTWSQ 236	Qy	
Db 179 - LGDLSEVELTRNNELIAGKSSLRKLPFGTEEVLFNLPHANGOKIVOTWSQ 236	Db	
Qy 239 CSKTCGTGISTRVTNDNPECRLVKTRICRVEPRCCQPVYSSIKKKCSKTKSKSPEPVRF 298	Qy	
Db 237 CSKSCGTGISTRVTNDNPECRLVKTRICRVEPRCCQPVYSSIKKKCSKTKSKSPEPVRF 298	Db	
Qy 299 TYAGCLSVKKYRPKKGSCUDRCRCCPQLRTVKMRFRCEDGEMFSKNVMMIQSCRNIN 356	Qy	
Db 297 TYAGCSSVKKYRPKKGSCUDRCRCCPQLRTVKMRFRCEDGEMFSKNVMMIQSCRNIN 356	Db	
Qy 359 CPHANEAAPFPYRLENDIKFRD 381	Qy	
Db 357 CPHNEASFLYSLENDIKFRD 379	Db	
RESULT 15		
ID ABB09201		
XX ID ABB09201 standard; protein: 379 AA.		
AC ABB09201;		
XX DT 08-JUL-2002 (first entry)		
DE XX		
Mouse cyr61 CNN family protein sequence SEQ ID NO:11.		
KW Human; small CCN-like growth factor; SCGF; vulnary; osteopathic; gene therapy; muscle wasting disease; osteoporosis; wound healing; tissue regeneration; angiogenesis.		
OS XX		
Mus sp.		
XX OS		
US2002049304-A1.		
PN XX		
25-APR-2002.		
XX		
PP 14-MAY-2001; 2001US-0853625.		
XX PR 06-JUN-1995; 95US-0468847.		
PR 01-APR-1998; 98US-0053587.		
XX PA (HAST/) HASTINGS G A.		
PA (ADAM/) ADAMS M D.		
XX PI Hastings GA, Adams MD;		

XX
XX
WPI; 2002-382150/41.
XX
DR

XX
PT Novel isolated polynucleotide sequence encoding a human small CCN-like
PT growth factor, useful for treating muscle wasting disease, and
PT osteoporosis -
XX
PS Disclosure: Fig 2A-D; 33pp; English.

CC The present invention describes human small CCN-like growth factor
(SCGF). SCGF has pulmonary and osteopathic activities, and can be used
CC in gene therapy. The SCGF polypeptides and polynucleotides can be used
CC for treating muscle wasting diseases, and osteoporosis, and to stimulate
CC wound healing and tissue regeneration, to promote angiogenesis and to
CC stimulate proliferation of vascular smooth muscle and endothelial cell
CC production. The present sequence represents a CNN family protein which
CC is given in comparison with the human SCGF in the exemplification of the
CC present invention.

XX Sequence 379 AA.;

Query Match 91.6%; Score 1938; DB 23; Length 379;

Best Local Similarity 91.4%; Pred. No. 1.8e-140; Matches 350; Mismatches 9; Conservative 18; Indels 6; Gaps 2;

QY	1 MSSRTARALAVVTLHLTRIALSTCPAACHCPLAEPAKCAPGVGLVRDGCGCCKVCAKOL	60
	:	
Db	1 MSSSIFRTLAVAVTLLHLTRIALSTCPAACHCPLAEPAKCAPGVGLVRDGCGCCKVCAKOL	60
QY	61 NEDCCKTQPODHTKLICLEGINGASSTALKGICRADESEGRCPEYNSRIVQNGESFOPNCKIQ	120
Db	61 NEDCSKRTQPOCDHTKGLECNFGASSTALKGICRASEGRCEPCEYNSRIVQNGESFOPNCKIQ	120
QY	121 CTCIDQAVGSIPLCQELSLPNLGCPNPRLVKVQGCCCCWCNCDSDIKPMDODGILG	180
	:	
Db	121 CTCIDQAVGSIPLCQELSLPNLGCPNPRLVKVQGCCCCWCNCDSDIKPMDODGILG	180
QY	181 KELGFDASEVELTRNNELLAVGKGSSLKKLRPVFGNEPRILYNPL-QGKRCIVQTTSWSQ	238
Db	179 --LGDADESVELTRNNELLAVGKGSSLKKLRPVFGNEPRILYNPL-QGKRCIVQTTSWSQ	236
QY	239 CSKTCTGTISTRVTNDNPCCRVLKTRTRICEVRPCCQPVVSSILKKKKCTTKSPEPVRF	298
Db	237 CSKSGCTGTISTRVTNDNPCCRVLKTRTRICEVRPCCQPVVSSILKKKKCTTKSPEPVRF	296
QY	299 TYAGCLSVKVKYRKPKCGCYDGRCTPQLTRTVKURFRCEDGETFSKKNMVIOSCKCNVN	358
Db	297 TYAGCSSLVKYRKPKCGCYDGRCTPQLTRTVKURFRCEDGETFSKKNMVIOSCKCNVN	356
QY	359 CPHANEAAFPYRLENDIHKFRD	381
	:	
Db	357 CPHPNFAFRYLSDENDIHKFRD	379

Search completed: July 8, 2003, 12:28:53
Job time : 72 secs

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OM protein - protein search, using sw model.

Run on: July 8, 2003, 12:26:17 ; Search time 40 Seconds

Sequence: 1 MSSRIRALALNVVILHLTR..... ANEAAPPFYRLFNDIHKFRD 381
(without alignments)

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Title: Perfect score: US-09-901-910-2

Score: 2115
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR_73;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1938	91.6	379	2 A35669	gene CYR61 protein CEF-10 protein pre beta Ig-M2 protein connective tissue NOV protein - chick gene novH protein hypothetical prote hypothetical prote Bablani ring 3 pr MEG3 protein - rat mucin-like peptide thrombospondin pre zonadhesin - mouse laminin Blk chain hypothetical prote protein F40E10.4 [notch4 - mouse secreted leucine-r mucin - rat hypothetical prote mucin, submaxillary mucin 2 precursor, notch protein - fr mucin 5AC (clone L cysteine-rich prot transmembrane Prot notch protein homotensin-X - bovin adhesive plaque pr
2	1699	80.3	375	2 A41428	
3	956.5	45.2	348	2 A40578	
4	951.5	45.0	349	2 A40551	
5	855.5	40.4	351	2 S20078	
6	834.5	39.5	357	2 T38069	
7	175.5	8.3	1620	2 T27283	
8	174	8.2	1111	2 T26972	
9	159	7.5	1700	2 T08167	
10	156	7.4	1574	2 T13954	
11	153	7.2	837	2 A42112	
12	152.5	7.2	1178	1 A39804	
13	152	7.2	1034	2 T42215	
14	147.5	7.0	1170	2 A53612	
15	145	6.9	601	2 T22025	
16	145	6.9	601	2 T09711	
17	144	6.8	1964	2 T09059	
18	142	6.7	1025	2 T42626	
19	141.5	6.7	1034	2 A5598	
20	141	6.7	1101	2 T16840	
21	141	6.7	13280	2 T03099	
22	141	6.7	2080	2 A43932	
23	140.5	6.6	2703	1 A24420	
24	139	6.6	1042	2 A57534	
25	138	6.5	251	2 A55035	
26	138	6.5	2437	2 S42612	
27	136	6.4	218188	2 A4135	
28	136	6.4	4135	2 T42629	
29	6.4	473	2 A56175		

ALIGNMENTS

RESULT 1	A35669	gene CYR61 protein precursor - mouse
C;Species:	Mus musculus (house mouse)	
C;Name:	gene CYR61	
C;Accession:	28-Sep-1990 #sequence_revision	18-Nov-1992 #text_change
R;O'Brien, T.P.; Yang, G.; Sanders, L.; Lau, L.F.		
Mol. Cell. Biol. 10, 3569-3577, 1990		
A;Title:	Expression of CYR61, a growth factor-inducible immediate-early gene.	
A;Reference number:	A35669;	MUID:90287146; PMID:2355916
A;Accession:	A35669	
A;Status:	preliminary	
A;Molecule type:	mRNA	
A;Residues:	1-379 <OAB>	
A;Cross-references:	GB:M32490; NID:9192909; PIDN:AAA37512.1; PID:q309206	
R;Latinkic, B.V.; O'Brien, T.P.; Lau, L.F.		
Nucleic Acids Res. 19, 3261-3267, 1991		
A;Title:	Promoter function and structure of the growth factor-inducible immediate early gene.	
A;Reference number:	I48319; MUID:91288203; PMID:2062642	
A;Accession:	I48319	
A;Status:	translated from GB/EMBL/DBJ	
A;Molecule type:	DNA	
A;Residues:	1-379 <RES>	
A;Cross references:	EMBL:X55790; NID:950632; PIDN:CAA40109.1; PID:950633	
A;Note:	the authors did not translate the codon for residue 108	
A;Note:	the authors did not translate the codon GAT for residue 337 as GIN	
C;Genetics:		
A;Gene:	CYR61	
A;Introns:	21/3; 93/1; 208/1; 279/3	
C;Superfamily:	von Willebrand factor type C repeat homology	
F9;99-166/Domain:	von Willebrand factor type C repeat homology <VWC>	
Query Match	91.6%	Score 1938; DB 2; Length 379;
Best Local Similarity	91.4%	Pred. No. 4.5e-15; Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2;

QY	1	MSSRIRALALNVVILHLTRALSTCPAACHCPEAKPCAPGVGLVRDGCGCKVCAKOL 60
Db	1	MSSSIFTLAVAVILHLTRALSTCPAACHCPEAKPCAPGVGLVRDGCGCKVCAKOL 60
QY	61	NEDCSKTQPCDHKGKLECNFGASSTALKSICRAOSEGRCEYNSRYONGESFOPNCKHO. 120
Db	61	NEDCSKTQPCDHKGKLECNFGASSTALKSICRAOSEGRCEYNSRYONGESFOPNCKHO. 120
QY	121	CTCTGDAVGSCTPICPQQLSLPNIGCPNPRLVKYTGQCRREWYEDSDIKPMDQDGIG 180
Db	121	CTCTGDAVGSCIPICLHQELSPNLNPRLVKYVGQCEEWCDSDIKSLDSLDD- 178
QY	181	KELGDAEVELTRNNELTAVGKSSLKLRLPVFGMPEPLYNPL-QGOKCIQVTSMSQ 238
Db	179	--LGDAEVELTRNNELTAVGKSSLKLRLPVFGMPEPLYNPL-QGOKCIQVTSMSQ 238

RESULT 2

A41428 protein precursor - chicken
 CEF-10
 C;Species: Gallus gallus (chicken)
 C;Cross-references: A41428; MUID:89145206; PMID:2537491
 C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jul-2000
 R;Simmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R. L.
 Proc. Natl. Acad. Sci. U.S.A. 86, 1778-1782, 1989
 A;Title: Identification of a phorbol ester-repressible v-src-inducible gene.
 A;Reference number: A41428; MUID:89145206; PMID:2537491
 A;Accession: A41428
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-375 <SIM>
 A;Cross-references: GB:J04496; NID:9211435; PIDN:AAA48661.1; PID:9211436
 Query Match Best Local Similarity 80.3%; Score 1699; DB 2; Length 375;
 Matches 312; Conservative 19; Mismatches 41; Gaps 7;
 QY 1 MSSRIRALARALVLTILHLTRL-STCPAACHCPLADPKCAPGVLVRDGCCKVCAQ 59
 Db 1 MSAGARP-ALAALCLARALAGSPCPAVCQCPAAAPQACPGVLYPDGCGCKVCAQ 59
 QY 60 LNEDCSKTOPCDHMKGLCNCNGASSTALKGICRAQSEGRCPEYNRSRYONGESFOPNCKH 119
 Db 60 LNEDCSKTOPCDHMKGLCNCNGASSTALKGICRAQSEGRCPEYNRSRYONGESFOPNCKH 119
 QY 120 QCICIDGAVGCPPLCPOELSLPMLPGCPUPRLVYKTGOCCEWQDDESIKDPMEDQCLL 179
 Db 120 QCICIDGAVGCPPLCPOELSLPMLPGCPUPRLVYKTGOCCEWQDDESIKDPMEDQCLL 179
 QY 180 GRELGFDAEVELTRNNELIAVKGSSKLRLPVFGMD--RILYNPLQGQKCTVQQTWS 237
 Db 178 SKEFGDASEGEITRNNEELIAVKG--GLKMLPVFGSEQSRAFENP---KCIVQTWS 232
 QY 238 QCSKTCGGIGSTRVTNDNPCLVKETRICEVPGQPVYSSLKKGKCSKTKSPEPV 297
 Db 233 QLSKTCGGIGSTRVTNDNPCLVKETRICEVPGQPVYSSLKKGKCSKTKSPEPV 292
 QY 298 FTYAGCLSVKVKRKYKPGCSCVGRCCTPQLTRIVKMRKRCDEGETFSKNNMMIQSCCKNY 357
 Db 293 FTYAGCLSVKVKRKYKPGCSCVGRCCTPQLTRIVKMRKRCDEGETFSKNNMMIQSCCKNY 352
 QY 358 NCPHANEAAFPVRLFLNDIKFRD 381
 Db 353 NCPHANEAAFPVRLFLNDIKFRD 375

RESULT 3

A40578 beta Ig-M2 protein precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Accession: A40578; A53228
 R;Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A. F.
 DNA Cell Biol. 10, 223-300, 1991
 A;Title: Identification of a gene family regulated by transforming growth factor-beta.
 A;Reference number: A40578; MUID:91229699; PMID:202837

RESULT 4

A40551 connective tissue growth factor - human
 C;Species: Homo sapiens (man)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
 C;Accession: A40551; S44205
 R;Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
 J. Cell Biol. 114, 1285-1294, 1991
 A;Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vascular smooth muscle cells
 A;Reference number: A40551; MUID:91373462; PMID:1654338
 A;Accession: A40551
 A;Molecule type: mRNA
 A;Residues: 1-349 <BRA>
 A;Cross-references: GB:N92934; GB:M36965; GB:S56201; NID:9180923; PIDN:AAA91279.1; PID:9474933
 R;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
 submitted to the EMBL Data Library, April 1994
 A;Description: Differential cloning and expression of human connective tissue growth factor
 A;Reference number: S44205
 A;Accession: S44205
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-349 <OEM>
 A;Cross-references: EMBL:X18947; NID:9474933; PID:9474934

Query Match Similarity 45.0%; Score 951; DB 2; Length 349;
 Best local similarity 46.9%; Pred. No. 1..3e-62; Mismatches 101; Indels 40; Gaps 8;
 Matches 175; Conservative 57; Mismatches 101; Indels 40; Gaps 8;

Db 208 EWSACKSKCGMGFSTRVTRNNQOCMVKQTRLCMRPCNEEPESD-KKGKCIQTKKSMR 266
 Qy 295 PVRITYAGGLSVKVKPRKGSCVUDGRCCPTQLTRTKMRFCEDGEFSKNMMIOSCK 354
 Db 267 AVRREYKNOTSVOKYPRGGIONDGRGCTPHNTKTOVERPQGKTIKKPMILINCV 326
 Qy 355 CNYNCOPHANEAF 367
 Db 327 CHGNCPQSNMAFF 339

Db 11 VAFVVLALACSRPAVGQNCSPGCRCPDEPAPRCPAGVSLVLDGCGGCCRCAKOLQECK 66
 Qy 67 TQPCDHTKOLECNFGASSTALKGICRAOSEGRCEYNRSRIVQESFOPNCKHQCTCIG 126
 Db 71 RDPCCDPHKGLFCFGSPANKTGVCYTAK-DGACBTGEGTYVRSSESFSCKYQCTCIG 129
 Qy 127 AVGCIPCLCPOELSLPLNPGCPNPRLVKVTGQCCBEWVCDDBSIKDPMEDODGGLGKELGFID 186
 Db 130 AVGCMPLCSCMDVRLPSPPDPFPFRVKLPGKXCEEWVCDP-----KDO----- 172
 Qy 187 ASEVELTRNELLAVGKQSSKLRL-PVIGMEPRLYNPLQGOKCIVOTTWSOCKTGTG 245
 Db 173 -----TIVGPAALAYRLEDTFGPDPTM-----RANCLVQPTFWSACKTCGM 215
 Qy 246 GISRTVNNDNPCECLVKERTRICEVVRPCGCPVYSSLLKKGKCSKITKSPBPVRYTIGCIS 305
 Db 216 GISRTVNNDNPCECLVKERTRICEVVRPCGCPVYSSLLKKGKCSKITKSPBPVRYTIGCIS 275
 Qy 306 VKKVPRPKYCGSCVDRGRCCTPQLTRVKMFERCEDGETFSKNNMIIQSCKCNYCNPANEA 365
 Db 275 MKTRAKFEGCVTPDRCCPFPHRTTLPVEFKCFDGEVNMKNMFPIKTCACHYNGPGNDI 335
 Qy 366 AFPEY--RFNFI 376
 Db 336 FESLYVYRKMYGDM 348

RESULT 5

S20078 NOV protein - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
 C;Accession: S20078
 R;Isolate: V.; Martinerie, C.; Dambrene, G.; Plassart, G.; Brisac, M.; Crochet, J.; Perrin, Cell. Biol. 12, 10-21, 1992
 A;Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in myeloid cell lines
 A;Reference number: S20078; MUID: 92107157; PMID:1309586
 A;Accession: S20078
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-351 <RES>
 A;Cross-references: EMBL:X78351; NID:9587422; PIDN:CAA55146.1; PID:9825696
 C;Genetics:
 A;Gene: novH
 A;Introns: 28/3; 104/1; 188/1; 259/3
 C;Superfamily: thrombospondin type 1 repeat homology <THR1>
 F;203-250/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match Similarity 39.5%; Score 834.5; DB 2; Length 357;
 Best Local Similarity 44.0%; Pred. No. 4.7e-54; Mismatches 48; Mismatches 160; Conservative 48; Mismatches 160;
 Matches 160; Conservative 48; Mismatches 160; Indels 39; Gaps 8;
 Matches 160; Conservative 48; Mismatches 160; Indels 39; Gaps 8;

Db 14 OCCLCTFLFLHLQGQAATQRCPQQCPGRCPATPTCAPGVRAVLGDGCSCLVCAQRQGE 73
 Qy 63 DCSTWQPCHTKGICRAOSEGRGEPEYNSRIVQESFOPNCKHQCT 122
 Db 74 SCSDLEPCDDESSGLYCDRSADPSNQNTGICTA-VEGDNCVFDGVYRSGEKFQPSCKEQT 132
 Qy 123 CIDGAVGCIPLCPOELSLPLNPGCPNPRLVKVTGQCCBEWVCDDBSIKDPMEDODGGLKE 182
 Db 133 CRDQGCVPRQCDLQDYLPEPNPAPKVEPEBCCKWIGD-----EDS185
 Qy 183 LGFDAESEVELTRNELLAVGKQSSKLRLPVFGMERRLYNPLQGOKCIVOTTWSOCKT 242
 Db 186 LA--AYRPATLGVF---SDSSV-----NCIEQTETWACKS 219
 Qy 243 CGTGISTRTVNNDNPCECLVKERTRICEVVRPCGCO-PVYSSLLKKGKCSKITKSPBPVRYA 301
 Db 220 CGMGFSTRVTRNNRNRQCEMLQTRLCKMVRPCCEOPEOPTDKKGKLRKLSKAHLQF 279
 Qy 302 GCLSVKVKPRKGSCVDRGRCCTPQLTRVKMFERCEDGETFSKNNMIIQSCKCNYCNPANPH 361
 Db 280 NCTSHRTYKPRFCVCSDCRCCTHNTKIQAEQCSPOQIVKPVMTIGTCCHTNCPK 339
 Qy 362 ANEA 365
 Db 340 NNEA 343

RESULT 7

T27283 hypothetical protein Y64G10A.f - Caenorhabditis elegans
 C;Species: Caeorhabditis elegans
 C;Accession: T27283
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 R;Ainscough, R.

Qy 181 -----KELGFDASSEVELTRNELLAVGKQSSKLRLPVFGMERRLYNPLQGOKCIVOTTWSOCKT 234
 Db 183 AAYRQEATLGVFSD-----SSANCIEQT 207
 Qy 235 SWSOCSKTCGTCGSPRVTRNNDNPCECLVKERTRICEVVRPCGCPVYSSLLKKKCSKT 294

submitted to the EMBL Data Library, September 1999

A; Reference number: Z20336

A; Accession: T27283

A; Status: preliminary; translated from GB/EMBL/DDJB

A; Molecule type: DNA

A; Residues: 1-1620 <WIL>

A; Cross-references: EMBL:AL11098; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f

C; Genetics:

A; Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 8.3%; Score 175.5; DB 2; Length 1620;

Best Local Similarity 24.2%; Pred. No. 5.2e-05; Matches 92; Conservative 33; Mismatches 146; Indels 109; Gaps 21;

Db 26 CPAAACHCPEAP-----KCAGP-----VGLVRPGCGCCWKCAKOLNECSK 66

Qy 1052 CKGICSCONGATCDSVTGSCCECPGRWRKRCDRCPDG---RFGECNAICDCMPTNDTSM 1109

Db 67 TQP--CDHTKGLECNFGFASSTALKGICRAQSEGRPQEYNSRIVQNGESFPQNCKQCT 122

Db 1110 YNPFWARCDDHVIG-ECR-----C-PAGMTGPQDGTSCPLGIGRE---GCRHSCQ 1153

Qy 123 C1DGAVGCLPLCPOEBSLNLGNLGPNPRLVKVTQGCCERWCDDSIKDPMEDODGLLGKE 182

Db 1154 CSNGA----SCDRVTGF---CDCPGFMKNCSECECPGGLWGSNCMKHLCMHGECNKE 1206

Qy 183 LGFDASEVELTRNELLWGKSSLKRKPVFGHEPRYLNPLOGOKCIVQT-----TSW 236

Db 1207 NG-----DCECIDGWTGPSLCPPQFGFRNCAQRNCINGASCDRKRTGRCECLPGW 1256

Qy 237 S---QCSKQCGTGISTRVNTNDPCLVKETRICEVRPGQQPVYSSLK---KGKKSKT 289

Db 1257 SGHECEKSCVSG----HYGAKC---EETCECENGALCDPITSGHCSCPGMRGKKNRNP 1307

Qy 280 KKSPEPVRETYAGLSSVYKRPYCG-----SC-VDGRGCTPQLIRTVKMRFRC 338

Db 1308 -----CL---KGYFGRHCSDSRCANSKSDHISGRQCPCPKYAGHSCTELCP 1352

Qy 339 DGEPFSKNVNMIIOSCKCNYN 358

Db 1333 DG-TPGESCS -OKDCGEN 1369

RESULT 8
T26972 hypothetical protein y47H9C.4 - *Caenorhabditis elegans*

C; Species: *Caenorhabditis elegans*

C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C; Accession: T26972

R; Harris, B.

submitted to the EMBL Data Library, October 1998

A; Reference number: Z20293

A; Accession: T26972

A; Status: preliminary; translated from GB/EMBL/DDJB

A; Molecule type: DNA

A; Residues: 1-111 <WIL>

A; Cross-references: EMBL:AL032657; PIDN:CAA21739.1; GSPDB:GN00019; CESP:y47H9C.4

A; Experimental source: clone Y47H9C

C; Genetics:

A; Gene: CESP:y47H9C.4

A; Map position: 1

A; Intron: 50/2; 84/2; 150/1; 238/3; 342/3; 797/1; 851/1; 947/2; 1017/1; 1083/1

C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 8.2%; Score 174; DB 2; Length 111;

Best Local Similarity 20.6%; Pred. No. 4.6e-05; Matches 87; Conservative 30; Mismatches 164; Indels 142; Gaps 20;

Qy 26 CRAPCHPEL-APKCAPGVGLYR----DGCCCKYCAK-QLNED-SKTQPDHTKGLE 78

Db 380 CSRTCTCVENTILMCAPNTGFCRKPKPGYGDNCALACSKDSYGPNCERQAMCDWNHASEC 439

Qy 79 NFGASTALKGICRAQSBRCPBINSRIVQNSFDFONKHOCTC-----IDGA----- 127

Db 440 NPFTGSC ---VCKPGRGKNCSEPCPL---DFYGCNAHCOCINORGVGCGDKCQ 491

Qy 128 -----NPRLVYKUTGOCCEEWVCDSDISIKDPMEDODGLLGKELGDFASVELT 193

Db 492 CDRGWTGHRCEHHCPADTFGANCEKRCCKPKGIGCDPITGETCPAGLQGANCDGPEG 551

Qy 147 -----NPRLVYKUTGOCCEEWVCDSDISIKDPMEDODGLLGKELGDFASVELT 193

Db 552 SYCPGCKLHKCKCYNGKCDKETGEC-----TC-----QPGFFSDCDCSTC5GKYG 596

Qy 194 RNNELIAVKGSSLKLRUPVFGMEPRILYNPLQGKCIYQT-TWSQSKTCGTG---IS 248

Db 597 ESCELSPCSDASCASK-----OTGKCLCPLGTRGVSDQKCDPNTFQLC 641

Qy 249 TRYNDNPECRLVKETRICEVRPGCQPVYSSLLKKKCSKTKSPERVRFTYAGCISVKK 308

Db 642 QETVTPSSCASTDPKNGVCLSCPPS---SGIHCENH-----PAGSYDGCCQV--- 688

Qy 309 YRPRKYGSCVDGRCCTQTLTRTV-----KMRFRGDEGETFSKNMMTQSKCNCNQ 360

Db 689 -----C-SCADGIGCDCPDTGECICPGYHGKPCSEKDGGKIGYGAALDCPKCASSSTD 742

Qy 361 HAN 363

Db 743 HIN 745

RESULT 9
S08167

Balbiani ring 3 Protein - midge (*Chironomus tentans*)

C; Species: Chironomus tentans

C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000

C; Accession: S08167

R; Paulsson, G.; Lendahl, U.; Galli, J.; Ericsson, C.; Wieslander, L.

J. Mol. Biol. 211, 331-349, 1990

A; Title: The balbiani ring 3 gene in *Chironomus tentans* has a diverged repetitive str

A; Reference number: S08167; MUID:90172404; PMID:1089777

A; Status: not compared with conceptual translation

A; Molecule type: DNA

A; Residues: 1-1700 <PRU>

A; Cross-references: GB:X52263; NID:g7057; PIDN:CAA36505.1; PID:g7058

C; Genetics:

A; Gene: BR3

C; Superfamily: unassigned Balbiani ring proteins

Query Match 7.5%; Score 159; DB 2; Length 1700;

Best Local Similarity 21.4%; Pred. No. 0.00088; Matches 90; Conservative 46; Mismatches 169; Indels 116; Gaps 22;

Db 30 CHPEALP-----CAGVGLVRDAGCG---CVCARQLNECSKQPCDHPKGLC-----NFG 81

Qy 221 CICPTAEPAGGGSAPLKDDDKCSCACPAKMEKEKKCVCESGKWIWNPNTECGCAOLCP 280

Db 82 ASSTALKGICRAQ-SEGRPCCENSRIVQNGESFPQPKHQPCCI----- 124

Db 281 DNKRANKETCQECCKEVRC-----NGGQF---CKDSCSGCVCPGGDKDRTCTAQVY 330

Qy 125 DGAVGCLPLCPOEBSLNLGNLGPNPRLVKVTQGCCERWCDDSIKDPMEDODGLLGKE 184

Db 331 DG-VACSCSPVNVMQKAADGCPDR-----QKWDKECRCEPK-HDCCKWVHD 378

Qy 185 FDASEVELTRNELLWGK---GSS-----IKRLPFGMPEPRYLPLQGKCIYQT 236

Db 379 ETICCICIPRDPAVCTAGKERGEGSCCECKCINREPREGCAKPLWVNE-NTCKCVCPADK- 436

Qy 237 SQCSKQCGTGISTRVNTNDPPEC-----RLVETRICEVRP-----CGOPVYSS 280

Db 437 QMSPGCGSGKSFNKLTQCOEQDQSASKGLRKRNADTCKCECOPMPPECGKQWISD 496

RESULT 10

QY 281 KKGKKCSKT-----KKSPEPVRFETACCLSVKKRP--- 311
| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 497 KCKCECSPTTCQAPQIIDLNVTECKCPVNMLAQEKCKSPHQWTDKCLCSTTATC 556
| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 312 ---KYCG--SCV---DGRCTPQLRTVKMRFRCEDGET-FSKNMVMTIOSCKNYNC 359
| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 557 ECKQTWGEACOCICPGDKNGKFKFDKPSCECKRKNNTCTSPQWDAADDCC-KC 614
| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
QY 360 P 360
Db 615 P 615

MEGF6 protein - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: 214126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-1574 <XUL>
A;Cross-references: EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3449294
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6

Query Match 7.4%; Score 156; DB 2; Length 1574;
Best Local Similarity 19.4%; Pred. No. 0.0012; Gaps 24;
Matches 89; Conservative 39; Mismatches 138; Indels 192; Gaps 24;
Matches 97; Conservative 37; Mismatches 132; Indels 176; Gaps 28;

QY 25 TCPA-----ACHCPLAEPKCPCVGVLVRDGGC--- 52
Db 419 TCPAHROYOAGCRSEPTCQSSPKRNSTLVEGCRCPEGITKFARPGYDVCKTGCVGD
QY 53 -----CKVC-----AKOLNEECSKTRQCDH 72
Db 479 NVPREFGEHEFFDCKDCVCLLEGSGCIVCPKCKARGNLTCEDGYLSVADDDKCCN 538
QY 73 TKGEBCN-----FGASSTALKGICRAQESEGRP--CEYNRIYONGESFOP 115
Db 539 TSCKCDPKRKKAERPSCLIGFEVKSERVHPGKCCPVSYGVCHENAEVYQPGSPVY 598
QY 116 NCKHOCTCID-----GAVGC--IPLCPOELSLPNLCCPNP-RLVKTTGCCBEWCD 164
Db 599 NKQCDQCVCPMSMDNSTOLNVNISCHVPG-----NICSGEELVPERGCKKCQDT 650
QY 51 GCKVKVAKQL-----NEDESKTPQCDHTKGLECNFGASSPAKGICR 92
Db 628 GAC-LCDPGLYGRFCHLACPWRAGPSCSEDCLCQ---SHTRSCKNPKDGS-----CK 678
QY 93 AOSEGRCEYINSRIVQNCESFOPNCVKHCTCIDGANGCIPL-----CPO 136
Db 679 AGFQGERCQAEQ---ESG-FEGPGCIRHCTCQPG-WACDPVSGECTQCOPPGYQGDQGQ 733
QY 137 ELSLPLNLG-----CNPRLVKTQOC-CSEWVCDBDSTIKPMEDODGLGKRELGFDA 187
Db 734 ECPVGTFGVNCGSCSCVCGAPCHRVTGECGLCPGKIGDGCADCPEGRWGLGCQEI--- 789
QY 188 SEVELTRNNELAVKGKSSLKRPLVFGEMEPRTILYNNPLGOKCIVOTITWSQSCKTC--- 243
Db 790 -----CPACEHGASC-----NPENGTCCLPFGVGSRCODTCAGW 825
QY 244 -GTGISTR-VTNNDPECRPLVKETRICEVRPPCQPVVSSLKKKKCSRTKKSPEPVRFTY 300
Db 826 YGPQGQRCACANDG-HCDPTTGRCSC-----APGWLGSQCORADSGHWD----- 872
QY 301 AGCLSLVKYRKPCK---GSC--VDGRC-CT---POLRTVKMRF--RCEDGETFSK 345
Db 873 -CI----HPCNCAGHGNCDAVSGLCLCEAGYEGPRCEOSCRQGYGPSC----- 918
QY 346 NYVMIQSKCNYN--CPHANE 365
Db 919 -----QKCRCEHGAAACDHVSGA 935

RESULT 11

MEGF6 protein - rat

C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Oct-1997
C;Accession: A42112
R;Xu, G.; Huan, L.J.; Khatri, I.A.; Wang, D.; Bennick, A.; Fahm, R.E.; Forstner, G.G.;
J. Biol. Chem. 267, 5401-5407, 1992
A;Title: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide
A;Reference number: A42112; MUID:92184794; PMID:1371999
A;Accession: A42112
A;Status: preliminary
A;Type: nucleic acid; protein
A;Residues: 1-837 <XUL>
A;Experimental source: intestine
A;Note: sequence inconsistent with the nucleotide translation
C;Superfamily: von Willebrand factor type C repeat homology
F;582-650/Domain: von Willebrand factor type C repeat homology <WVC>
A;Note: sequence extracted from NCBI backbone (NCBIP:87420)

Query Match 7.2%; Score 153; DB 2; Length 837;
Best Local Similarity 19.4%; Pred. No. 0.0012; Gaps 24;
Matches 89; Conservative 39; Mismatches 138; Indels 192; Gaps 24;
Matches 97; Conservative 37; Mismatches 132; Indels 176; Gaps 28;

QY 25 TCPA-----ACHCPLAEPKCPCVGVLVRDGGC--- 52
Db 419 TCPAHROYOAGCRSEPTCQSSPKRNSTLVEGCRCPEGITKFARPGYDVCKTGCVGD
QY 53 -----CKVC-----AKOLNEECSKTRQCDH 72
Db 479 NVPREFGEHEFFDCKDCVCLLEGSGCIVCPKCKARGNLTCEDGYLSVADDDKCCN 538
QY 73 TKGEBCN-----FGASSTALKGICRAQESEGRP--CEYNRIYONGESFOP 115
Db 539 TSCKCDPKRKKAERPSCLIGFEVKSERVHPGKCCPVSYGVCHENAEVYQPGSPVY 598
QY 116 NCKHOCTCID-----GAVGC--IPLCPOELSLPNLCCPNP-RLVKTTGCCBEWCD 164
Db 599 NKQCDQCVCPMSMDNSTOLNVNISCHVPG-----NICSGEELVPERGCKKCQDT 650
QY 51 GCKVKVAKQL-----NEDESKTPQCDHTKGLECNFGASSPAKGICR 92
Db 628 GAC-LCDPGLYGRFCHLACPWRAGPSCSEDCLCQ---SHTRSCKNPKDGS-----CK 678
QY 93 AOSEGRCEYINSRIVQNCESFOPNCVKHCTCIDGANGCIPL-----CPO 136
Db 679 AGFQGERCQAEQ---ESG-FEGPGCIRHCTCQPG-WACDPVSGECTQCOPPGYQGDQGQ 733
QY 137 ELSLPLNLG-----CNPRLVKTQOC-CSEWVCDBDSTIKPMEDODGLGKRELGFDA 187
Db 734 ECPVGTFGVNCGSCSCVCGAPCHRVTGECGLCPGKIGDGCADCPEGRWGLGCQEI--- 789
QY 188 SEVELTRNNELAVKGKSSLKRPLVFGEMEPRTILYNNPLGOKCIVOTITWSQSCKTC--- 243
Db 790 -----CPACEHGASC-----NPENGTCCLPFGVGSRCODTCAGW 825
A33804
QY 244 -GTGISTR-VTNNDPECRPLVKETRICEVRPPCQPVVSSLKKKKCSRTKKSPEPVRFTY 300
Db 826 YGPQGQRCACANDG-HCDPTTGRCSC-----APGWLGSQCORADSGHWD----- 872
QY 301 AGCLSLVKYRKPCK---GSC--VDGRC-CT---POLRTVKMRF--RCEDGETFSK 345
Db 873 -CI----HPCNCAGHGNCDAVSGLCLCEAGYEGPRCEOSCRQGYGPSC----- 918
QY 346 NYVMIQSKCNYN--CPHANE 365
Db 919 -----QKCRCEHGAAACDHVSGA 935

RESULT 12

thrombospondin precursor - chicken

C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A39804
R;Lawler, J.; Duquette, M.; Ferro, P.
J. Biol. Chem. 266, 8039-8043, 1991
A;Title: Cloning and sequencing of chicken thrombospondin.
A;Reference number: A39804; MUID:91217026; PMID:2022631
A;Accession: A39804
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1178 <LAW>
A;Cross References: GB:M60853; NID:g212763; PIDN:AAA51437.1; PID:g212764
C;Superfamily: thrombospondin 1; EGP homology; thrombospondin type 1 repeat homology <WVC>
F;325-383/Domain: von Willebrand factor type C repeat homology <WVC>
F;386-437/Domain: thrombospondin type 1 repeat homology <THR1>
F;442-498/Domain: thrombospondin type 1 repeat homology <THR2>

RESULT 11

A42112
mucin-like peptide MLP 2677 - rat

hypothetical protein F40E10.4 - *Caenorhabditis elegans* (fragment)
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;annotation: m205

R;SUYE, K.
submitted to the EMBL Data Library, February 1996
A;Reference number: 219503
A;Accession: T22025
A;Status: preliminary; translated from GB/EMBL/IDB/J
A;Molecule type: DNA
A;Residues: 1-601 <WIL>
A;Cross-references: EMBL:269792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
A;Experimental source: clone F40E10
C;Genetics:
C;cancer genes: F40E10

Glossy Watch

Best Local Similarity 19.8%; Pred. No. 0.003; Mismatches 93; Conservative 52; Mismatches 142; Indels 182; Gaps - 24;

Qy	Db	30 CHCPLRALKCABGVGLVRUDGCCG--CKVCAKOLNEDCSKTQPC----- 70
	162 CDCPME-----YEKGICKEDELYCTKRN PCENNGKCIPINGSYSCMSPGET	209

QY 71 -----DHTKGLECNFGASSTALKGI-----CRAOSEGRCPECYNSRI--YONGESF 113
| | : | | : || | | : | | : || | ::

Qy	Db
114 QPNCKHQ-----	210 GNNCTTIDCKNVECNGGS-----
	-CVDGITSYDCILCRPGYAGOTCEIIPPMMDMEYQTKDAC
	267
	148

Db 268 QOSACGECVAVSONSSDFTCKHEGFSG--PSCDRMS--vgKNPGAYLALDDPLASD 322
Qo 148

QY . 204 -GSSLKRLPVFGMPEPTLYN- -PLQQGOKCIVQTTSWSOCSTK- -CGRQISTRVY 252

QY	253	ND--NP <small>E</small> P <small>C</small> R <small>L</small> V <small>E</small> T <small>R</small> I <small>E</small> V <small>R</small> P <small>C</small> G <small>Q</small> P <small>V</small> V <small>S</small> L <small>K</small> K <small>O</small> K <small>K</small> C <small>S</small> K <small>T</small> K <small>S</small> P <small>E</small> P <small>V</small> R <small>E</small> T <small>Y</small> A <small>G</small> C <small>L</small> S <small>V</small> K <small>K</small> R	443	N <small>E</small> S <small>L</small> K <small>---</small> GC <small>I</small> S <small>T</small> T <small>I</small> N <small>E</small> W <small>P</small> I <small>N</small> L <small>Q</small> A <small>L</small> E <small>N</small> N <small>T</small> E <small>D</small> S <small>C</small> S <small>A</small> T <small>V</small> N <small>F</small> C <small>A</small> G <small>I</small> D <small>C</small> G <small>N</small> --K <small>O</small> T	494
----	-----	---	-----	---	-----

Db : 495 NNALSPKGMCQ--CDSHFSE--HCDEKKRICKDKOKFRRHIE--NECRSYDIRK 544

QY	311	-----PKKGSCVDRGCTPQLTRTVKMRFCGEGETFSKNNMIOQCK	355
Db	545	IAECNGYCGG - BQNCCATAVKKKQRKVKKMICKNGTTKISVHIIROCQC	591

Search completed: July 8, 2003, 12:31:40
Job time: 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model.

Run on: July 8, 2003, 12:13:12 ; Search time 23 Seconds

(without alignments) 687.064 Million cell updates/sec

Title: US-09-901-910-2

Perfect score: 2115

Sequence: 1 MSSRIRALALVVILHLTR.....ANEAAPPYRLFNDIHKFRD 381

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_40:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES ~

Result No.	Score	Query Match Length	DB ID	Description
1	2115	100.0	381	CYRG_HUMAN
2	1938	91.6	379	1 CYRG_MOUSE
3	1699	80.3	375	1 CYR6_CHICK
4	952.5	45.0	348	1 CTGF_MOUSE
5	931	45.0	349	1 CTGF_BOVIN
6	910	43.0	349	1 CTGF_PIG
7	855.5	40.4	351	NOV_CHICK
8	852	40.3	353	1 NOV_COTJA
9	834.5	39.5	357	1 NOV_HUMAN
10	829.5	39.2	343	1 NOV_XENLA
11	823	38.9	354	1 NOV_MOUSE
12	819	38.5	1700	1 BAR3_CHWHITE
13	153	7.5	837	1 MUC1_RAT
14	152.5	7.2	1178	1 TSP2_CHICK
15	152	7.2	5376	1 ZAN_MOUSE
16	151	7.1	3110	1 LMA2_HUMAN
17	148.5	7.0	2282	1 ZAN_RABIT
18	144.5	6.8	1172	1 LMB3_HUMAN
19	144	6.8	1964	1 NTC4_MOUSE
20	21	6.8	1173	1 TSP1_XENLA
21	143	6.8	5179	1 MUC2_HUMAN
22	141	6.7	2703	1 NOTC_DROME
23	140.5	6.6	1405	1 HRA3_HUMAN
24	138	6.5	453	1 NTCL_BRARE
25	138	6.5	2437	1 VWF_PIG
26	138	6.5	2482	1 VWF_PIG
27	137.5	6.5	480	1 HRA1_MOUSE
28	137	6.5	170	1 TSP1_BOVIN
29	137	6.5	1587	1 LMG3_HUMAN
30	136	6.4	2531	1 NTC1_RAT
31	135	6.4	2813	1 WVF_CANFA
32	135	6.4	473	1 FP2_MYTGA
33	1168	6.4	1168	1 LMB3_MOUSE

ALIGNMENTS

34	134	6.3	1056	1 MUC5_HUMAN	P98088 homo sapien
35	134	6.3	1218	1 JAG1_MOUSE	Q9qxx0 mus musculu
36	134	6.3	2871	1 FBNL_HUMAN	P35555 homo sapien
37	133.5	6.3	1106	1 STC_DROME	P4078 drosophila
38	133.5	6.3	1480	1 SLT7_DROME	P24014 drosophila
39	133.5	6.3	1955	1 AGRI_CHICK	P31696 gallus galli
40	133	6.3	460	1 HRA3_MOUSE	Q9d236 mus musculu
41	133	6.3	1170	1 TSPL_MOUSE	P35441 mus musculu
42	133	6.3	2813	1 WVF_HUMAN	P04275 homo sapien
43	133	6.3	3106	1 LMA2_MOUSE	Q60675 mus musculu
44	133	6.3	3672	1 LML2_CAEEL	P23133 caenorhabdi
45	131.5	6.2	703	1 FBL1_HUMAN	P23142 homo sapien

RESULT 1

CYRG_HUMAN	ID CYRG_HUMAN	STANDARD; PRT;	381 AA.
	AC 006622; 014934; 043775; 098217;		
	DT 15-JUL-1998 (Rel. 36, Created)		
	DT 15-JUL-1998 (Rel. 36, Last sequence update)		
	DT 15-JUN-2002 (Rel. 41, Last annotation update)		
	DE CYRG6 protein precursor (Cysteine-rich, angiogenic inducer, 61) (GIG1 protein) (Insulin-like growth factor-binding protein 10).		
	DE CYR61 OR IGFAP10 OR GIG1.		
	OS Homo sapiens (Human).		
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
	OC NCBI_TaxID:9606;		
	RN [1]		
	RP MEDLINE:972B0750; PubMed=9135077;		
	RA Jay P., Berge-Lefranc J.-L., Marsollier C., Mejean C., Taviaux S.,		
	RA Betty P.,		
	RA "The human growth factor-inducible immediate early gene, CYR61, maps to chromosome 1P." [3]		
	RP SEQUENCE FROM N.A.		
	RA MEDLINE:9819734; PubMed=9536281;		
	RA Marcellier C., Vegas-Arquianot E., Nguyen V.C., Perbal B.;		
	RT Chromosomal mapping and expression of the human cyr61 gene in tumour cells from the nervous system."; Mol. Pathol. 50:310-316(1997).		
	RP [4]		
	RP SEQUENCE FROM N.A.		
	RC TISSUE=placenta;		
	RC Kolesnikova T.V., Lau L.F.;		
	RA Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.		
	RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.		
	RN [5]		
	RP SEQUENCE FROM N.A.		
	RA Bi A.B., Yu L.;		
	RA Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.		
	RL [6]		
	RP SEQUENCE FROM N.A.		
	RA Schuetze N., Lechner A., Groll C., Koehrl J., Jakob F.;		
	RT "Regulation of hcyr61 by vitamin D, serum and cytokines in fetal human osteoblasts"; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.		
	RL [7]		
	RP SEQUENCE FROM N.A.		
	RA Leng E., Tai G., Estable M., Liu J., Chow C., Sadowski I.;		
	RT "Organization and expression of the CYR61 gene in normal human fibroblasts"; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.		
	RL [8]		
	RP SEQUENCE FROM N.A.		

RC TISSUE=lung, Placenta, and Skin;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
 PROTEINS; PROMOTES PROLIFERATION, MIGRATION AND ADHESION (BY
 CC SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -I- SIMILARITY: CONTAINS 1 WFPC DOMAIN.
 CC -I- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.

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CC

DR EMBL: Y12084; CAJ72802; 1;
 DR EMBL: U62015; ARB5319; 1;
 DR EMBL: Y11307; CAJ72167; 1;
 DR EMBL: AF003594; AAB61240; 1;
 DR EMBL: AF031385; AAB84227; 1;
 DR EMBL: 298053; CAD10848; 1;
 DR EMBL: AAF307860; AAQ59863; 1;
 DR EMBL: BCB01271; AAB01271; 1;
 DR EMBL: BCB009199; AAH09199; 1;
 DR GeneW: HGNC:2654; CYR61.
 DR MM: 602369; --.
 DR InterPro: IPR000359; CYS_knot.
 DR InterPro: IPR000867; Insl_gro_fac_pr.
 DR InterPro: IPR000884; TSP1.
 DR InterPro: IPR001007; WFP_C.
 DR Pfam: PF00007; Cys_knot; 1.
 DR Pfam: PF00053; vwc; 1.
 DR Pfam: PF00019; IGFBP; 1.
 DR SMART: SM00041; CT; 1.
 DR PROSITE: PS011225; CTCK_1; 1.
 DR SMART: SM00029; TSP1; 1.
 DR SMART: SM00314; WFC; 1.
 DR PROSITE: PS00022; IGF_BINDING; 1.
 DR SMART: SM00121; IB; 1.
 DR PROSITE: PS011225; CTCK_2; 1.
 DR SMART: SM00029; TSP1; 1.
 DR Growth factor binding; signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 381 CYR61 PROTEIN.
 FT DOMAIN 98 164 VWF.
 FT DOMAIN 286 360 CTCK.
 FT DISULFID 286 323 BY SIMILARITY.
 FT DISULFID 303 337 BY SIMILARITY.
 FT DISULFID 314 353 BY SIMILARITY.
 FT DISULFID 317 355 BY SIMILARITY.
 FT DISULFID 322 359 BY SIMILARITY.
 FT CONFLICT 165 165 E -> Q (IN REF. 3).
 FT CONFLICT 210 210 L -> I (IN REF. 5).
 FT CONFLICT 220 220 L -> R (IN REF. 5).
 FT CONFLICT 369 369 P -> L (IN REF. 7).
 FT SEQUENCE 381 AA; 42026 MW; FC0BD39C078CA0B1 CRC64;

Query Match 100.0%; Score 2115; DB 1; Length 381;
 Best Local Similarity 100.0%; Pred. No. 3; 3e-150;
 Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC MSSRIARALLALVYLTLHLRLSTCPAACHCPLEAPKACPARGVGLYRDGCCKVCAKQL 60
 1 MSSRIARALLALVYLTLHLRLSTCPAACHCPLEAPKACPAGVGLYRDGCCKVCAKQL 60
 CC 61 NEDCSKIQPCDITKGLECNFGASSTALKGICRAQSEGRCPEYNSRIVONGESFQPCKHQ 120
 CC
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 CC or send an email to license@isb-sib.ch).

Db 61 NEDCSKIQPCDITKGLECNFGASSTALKGICRAQSEGRCPEYNSRIVONGESFQPCKHQ 120
 QY 121 CTCIDGAVGCIPLCPOEQLSPNLPGPNCNPRLVKVPGQCEEWYQCDDESDIKDPMDQDLSLG 180
 Db 121 CTCIDGAVGCIPLCPOEQLSPNLPGPNCNPRLVKVPGQCEEWYQCDDESDIKDPMDQDLSLG 180
 181 KELGFDASEVELTRNLIAVKGSSLKRIPVFGMEPRLYNPLQGOKCVWOTWSQCS 240
 181 KELGFDASEVELTRNLIAVKGSSLKRIPVFGMEPRLYNPLQGOKCVWOTWSQCS 240
 241 KRCGTGISTRWINDNPECRLVKETRICEVRPGCQPVSSLKKKKCSKTKSPEPRFTY 300
 241 KRCGTGISTRWINDNPECRLVKETRICEVRPGCQPVSSLKKKKCSKTKSPEPRFTY 300
 301 AGCLSVKKYRKPKCSCGVGRCCTPQLRTVKMRPDEGETFSKNMAMIOSCKCNCP 360
 301 AGCLSVKKYRKPKCSCGVGRCCTPQLRTVKMRPDEGETFSKNMAMIOSCKCNCP 360
 QY 361 HANEAFFPYRLNDIHKFRD 381
 361 HANEAFFPYRLNDIHKFRD 381

Db QY 241 KRCGTGISTRWINDNPECRLVKETRICEVRPGCQPVSSLKKKKCSKTKSPEPRFTY 300
 QY 301 AGCLSVKKYRKPKCSCGVGRCCTPQLRTVKMRPDEGETFSKNMAMIOSCKCNCP 360
 Db 361 HANEAFFPYRLNDIHKFRD 381

CC CEF-10 protein Precursor.
 DR EMBL: M32490; AAA37512.1; -;
 DR X56790; CAA40109.1; -;
 DR PIR; A35669; A35669;
 DR MGD; MG1:88613; CYF61;
 DR InterPro; IPR00867; Insl_gro_fac_pr.
 DR InterPro; IPR00884; TSPI.
 DR Pfam; PF00007; Cys_knot; 1.
 DR Pfam; PF00090; tsp_1; 1.
 DR Pfam; PF00093; vwc_1.
 DR Pfam; PF00219; IGBFP; 1.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00121; IB; 1.
 DR SMART; SM00209; TSPI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00222; IGF BINDING; 1.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01208; WWFC; 1.
 KW Growth factor binding; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 379 CYR61 PROTEIN.
 FT DOMAIN 98 164 WWFC.
 FT DOMAIN 284 358 CTCK.
 FT DISULFD 284 321 BY SIMILARITY.
 FT DISULFD 301 335 BY SIMILARITY.
 FT DISULFD 312 351 BY SIMILARITY.
 FT DISULFD 315 353 BY SIMILARITY.
 FT DISULFD 320 357 BY SIMILARITY.
 SQ SEQUENCE 379 AA; 41709 MW; FAB65014B56ABEE9 CRC64;

Query Match 91.6%; Score 1938; DB 1; Length 379;
 Best Local Similarity 91.4%; Pred. No. 4.5e-137;
 Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2; C-terminal
 CC MSSRIARALAVLTLLHTRLSTCPAACHCPLAEPAKCAPGVGLVRDGGCCVKCAKLQ 60
 CC ||||| - |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MSSSFTRTLAVAVTLLHTRLSTCPAACHCPLAEPAKCAPGVGLVRDGGCCVKCAKLQ 60
 CC NEDCSKIQPCDHTKGLECNFGQASSTALKGICRAOSEGRCPEBYNSRIVYQNGESFQPNCKHQ 120
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 61 NEDCSKIQPCDHTKGLECNFGQASSTALKGICRAOSEGRCPEBYNSRIVYQNGESFQPNCKHQ 120
 Db 61 NEDCSKIQPCDHTKGLECNFGQASSTALKGICRAOSEGRCPEBYNSRIVYQNGESFQPNCKHQ 120
 Qy 121 CTCIDGAVGCIPLCPOEELSLPVLNPGPNNPRLVYKTSQCCSEEWCDSDSIKPPMEDQDGLLG 180
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||:
 Db 121 CTCIDGAVGCIPLCPOEELSLNLCNPNRLVKSGOCCEEWCDSDSIKPPMEDQDGLLG 180
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||:
 Db 121 CTCIDGAVGCIPLCPOEELSLNLCNPNRLVKSGOCCEEWCDSDSIKPPMEDQDGLLG-- 178
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||:
 Qy 181 KELGFDASEVELTRNLIELAVKGSSLRKLPVFGMPRLYNPL-QGQKCIQVOTSWSQ 238
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 179 --LGLDASEEVLTNLIELAVKGSSLRKLPVFGMPRLYNPL-HAGQKCIQVOTSWSQ 236
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 239 CSKTCCTGISTRVTNNDPNECRLVKETRICEYVRPGCOPVYSSLLKGKKCSKTKKSPPVRF 298
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 237 CSKSCGTGISTRVTNNDPNECRLVKETRICEYVRPGCOPVYSSLLKGKKCSKTKKSPPVRF 296
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Qy 299 TYAGCISVKYKRPKYCQGCGVGRCCPQLTYVKARFCEGETTSKVNMMIQSKCNYN 358
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 297 TYAGCISVKYKRPKYCQGCGVGRCCPQLTYVKARFCEGETTSKVNMMIQSKCNYN 356
 CC ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 3
 CC CEL0_CHICK
 ID CE10_CHICK STANDARD PRT; 375 AA.
 Db P19336; 01-NOV-1990 (Rel. 15, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE CEF-10 protein Precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; AVES; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8914206; PubMed=2537491;
 RA Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
 RT "Identification of a phorbol ester-repressible v-src-inducible gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:178-182(1989).
 CC -.- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
 CC -.- INDUCTION: BY V-SRC.
 CC -.- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYR61/CFGF/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -.- SIMILARITY: CONTAINS 1 WWFC DOMAIN.
 CC -.- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.
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 CC -.-
 DR PROSITE; PS00222; IGF BINDING; 1.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01208; WWFC; 1.
 DR PROSITE; PS00090; tsp_1; 1.
 DR Pfam; PF00093; vwc_1.
 DR Pfam; PF00219; IGBFP; 1.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00121; IB; 1.
 DR SMART; SM00209; TSPI; 1.
 DR PROSITE; PS00222; IGF BINDING; 1.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01208; WWFC; 1.
 DR Pfam; PF00093; vwc_1.
 DR Pfam; PF00219; IGBFP; 1.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00121; IB; 1.
 DR SMART; SM00209; TSPI; 1.
 DR PROSITE; PS00222; IGF BINDING; 1.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01208; WWFC; 1.
 KW Growth factor binding; Signal.
 FT SIGNAL 1 22 CEF-10 PROTEIN.
 FT CHAIN 23 375
 FT DOMAIN 98 164 WWFC.
 FT DOMAIN 281 355 CTCK.
 FT DISULFD 281 318 BY SIMILARITY.
 FT DISULFD 298 332 BY SIMILARITY.
 FT DISULFD 309 348 BY SIMILARITY.
 FT DISULFD 312 350 BY SIMILARITY.
 FT DISULFD 317 354 BY SIMILARITY.
 SQ SEQUENCE 375 AA; 40651 MW; 95F20553B35D5AE CRC64;

Query Match 80.3%; Score 1699; DB 1; Length 375;
 Best Local Similarity 81.2%; Pred. No. 2.5e-119;
 Matches 312; Conservative 19; Mismatches 41; Indels 12; Gaps 7;

CC MSSRIARALAVLTLLHTRLSTCPAACHCPLAEPAKCAPGVGLVRDGGCCVKCAKLQ 59
 CC ||||| - |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MGSAGARP-ALAALALCLARALGSP-PAVQCPAAAPQCAPGVGLVRDGGCCVKCAKLQ 59
 Qy 60 INEDCSKIQPCDHTKGLECNFGQASSTALKGICRAOSEGRCPEBYNSRIVYQNGESFQPNCKHQ 119
 Db 60 LNEDCSKIQPCDHTKGLECNFGQASSTALKGICRAOSEGRCPEBYNSRIVYQNGESFQPNCKHQ 119
 Qy 120 OCTCIDGAVGCIPLCPOEELSLPVLNPGPNNPRLVYKTSQCCSEEWCDSDSIKPPMEDQDGLL 179
 Db 120 OCTCIDGAVGCIPLCPOEELSLPVLNPGPNNPRLVYKTSQCCSEEWCDSDSIKPPMEDQDGLL 177
 DE CEF-10 protein Precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; AVES; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8914206; PubMed=2537491;
 RA Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
 RT "Identification of a phorbol ester-repressible v-src-inducible gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:178-182(1989).
 CC -.- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
 CC -.- INDUCTION: BY V-SRC.
 CC -.- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYR61/CFGF/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -.- SIMILARITY: CONTAINS 1 WWFC DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
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QY 357 YNCPHANEAAFPFY-RLENDI 376
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 ID CTGF_HUMAN STANDARD; PRT; 349 AA.
 AC P29279; O9QX2; DR;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Connective tissue growth factor precursor (Hypertrophic chondrocyte-specific protein 24).
 GN CTGF OR HCS24.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE="umbilical vein endothelial cells;"
 RX MEDLINE-9137462; PubMed-1654338;
 RA Bradham D.M., Igashii A., Potter R.L., Grotendorst G.R.;
 RT "Connective tissue growth factor: a cysteine-rich mitogen secreted by human vascular endothelial cells is related to the SRC-induced immediate early gene product CEF-10.", J. Cell Biol. 114:1285-1294(1991).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE="umbilical vein endothelial cells;"
 RX MEDLINE-93187114; PubMed-1223144;
 RA Igashii A., Bradham D.M., Okochi H., Grotendorst G.R.;
 RT "Connective tissue growth factor," J. Dermatol. 19:642-643(1992).
 RL [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE-97207446; PubMed-9054739;
 RA Oemar B.S., Werner A., Garner J.M., Do D.D., Godoy N., Nauck M., Marz W., Rupp J., Pech M., Luescher T.F.;
 RT "Human connective tissue growth factor is expressed in advanced atherosclerotic lesions"; Circulation 95:831-839(1997).
 RL [4]
 RN SEQUENCE FROM N.A.
 RA Cobley V.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP FUNCTION.
 RC TISSUE="chondrocytes;"
 RX MEDLINE-20080284; PubMed-10614647;
 RA Nakano T., Nishi T., Shimo T., Kobayashi K., Kubo T., Tamai T., Tezuka K., Takigawa M.;
 RT "Effects of CTGF/HCS24, a product of a hypertrophic chondrocyte-specific gene, on the proliferation and differentiation of chondrocytes in culture"; Endocrinology 141:264-273(2000).
 CC -!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND DIFFERENTIATION OF CHONDROCYTES.
 CC -!- FUNCTION: MEDIATES CELL ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SOLUBLE FORM (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM. SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CTFR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 VWFc DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CCTK) DOMAIN.

RESULT 5
 CTGF_HUMAN
 ID CTGF_HUMAN STANDARD; PRT; 349 AA.
 AC P29279; O9QX2; DR;
 DT 01-DEC-1992 (Rel. 24, Created)
 DE Connective tissue growth factor precursor (Hypertrophic chondrocyte-specific protein 24).
 GN CTGF OR HCS24.
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 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 OX NCBI_TAXID=9606;
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 RT "Effects of CTGF/HCS24, a product of a hypertrophic chondrocyte-specific gene, on the proliferation and differentiation of chondrocytes in culture"; Endocrinology 141:264-273(2000).
 CC -!- FUNCTION: MAJOR CONNECTIVE TISSUE MITOATTRACTANT SECRETED BY VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND DIFFERENTIATION OF CHONDROCYTES.
 CC -!- FUNCTION: MEDIATES CELL ADHESION AND ENHANCES FIBROBLAST GROWTH FACTOR-INDUCED DNA SYNTHESIS (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER.
 CC -!- SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SOLUBLE FORM (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM. SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CTFR61/CTGF/FISP-12/NOV PROTEIN SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 VWFc DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CCTK) DOMAIN.

Query Match 45 / 0%; Score 951; DB; 1; Length: 349;
 Best Local Similarity 46.9%; Pred. No. 8.2e+64; Gaps 8;
 Matches 175; Conservative 57; Mismatches 101; Indels 40; Gaps 8;

QY 9 LALVNTLHLTRLAL-STCPAACHPOLEAPKACPGVLYRDGGCKVKCAQLNEDCSK 66
 DR 11 VAFVWVIALCCSRPAVGQNCSCPCRCDEPAPRCPPAGVSLWDGCCCRVCAKQLGRCLTE 70
 QY 67 TQPCHIHKGLBCNFQASSTALKIGICQAQSEGRCPEVNSRIVONGSFQPNCKHQTCIDG 126
 DR 71 RDPCCDPHKGLCDFGSPANRKIGVCTAK-DGAPCFGGTVRSGESFQSCKYQTCIDG 129
 QY 127 AVGCITLCPQELSLPNUGCPMPRLVYTGCGCEEWVCDSESIKDMEDODGILGRELGD 186
 DR 130 AVGCMPLCSMDYVRPLSPDCPFPRRYVRLPKGCKCEEWVCDP-----KDQ----- 172
 QY 187 ASEVELTRNNELIAVGSSKRL-PVFGMPRLYLNPLQGQKC-VOTWSQSKTCGT 245
 DR 173 -----TVAQPALAAYRLTDFFGPDPTML---RANCILWOTTWMSACSKTCGM 215
 QY 246 GISTRVVNDNPFCRVLKRETICEVRPGQPVYSSKKKGKSKTKSPVRFYAGCLS 305
 DR 216 GISTRVVNDNPACRLEKQSRQLCMVRCFAEDELEENKKKGKQKIRTKISKPIEELSGCTS 275
 QY 306 VKKYRPKYCGSCVDGRCTPQLTTRVKMFRCEDTSFSKNVMMIQSCKCNVNCPHANE 365

RESULT 6

ID	CYCF_BOVIN	STANDARD;	PRT;	349 AA.
AC	Q18739; O9GL71;			
DT	13-JUL-1998 (Rel. 36, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Connective tissue growth factor precursor.			
GN	CYCF			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.			
OX	NCBI_TAXID=9913;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE_Korta;			
RA	Liu Z., Fotsis T., Schimanski M., Bierhaus A., Kanitz M., Kaufmann G., Schweigeler D., Ziegler R., Nawroth P.P.; Submitted (AUG-1997) to the EMBL/Genbank/DDBJ databases.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE_Liver;			
RA	M. Schwitters C., Hove M., Rupp S., Erondu N.E.; *Bovine connective tissue growth factor, organization of the chromosomal gene and demonstration of promoter activity.;			
RL	Submitted (SEP-2000) to the EMBL/Genbank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	VASCULAR ENDOTHELIAL CELLS. PROMOTES PROLIFERATION AND DIFFERENTIATION OF CHONDROCYTES (BY SIMILARITY).			
CC	-1- FUNCTION: REGULATES CELL ADHESION AND ENHANCES FIBROBLAST GROWTH			
CC	FACTOR-INDUCED DNA SYNTHESIS (BY SIMILARITY).			
CC	-1- SUBFUNCTION: MONOMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: FOUND IN THE EXTRACELLULAR MATRIX AND AS A SOLUBLE FORM (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYCF1/CTCF/FISP-12/NOV PROTEIN SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 WIFC DOMAIN.			
CC	-1- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE (CTCK) DOMAIN.			
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CC	[1]			
EMBL; AP000137; AAB6596; 1;				
EMBL; AP30955; AAG3090; 1;				
InterPro; IPR00059; Cys_knot.				
InterPro; IPR00067; insl_gro_fac_pr.				
DR	InterPro; IPR00084; TSP1.			
DR	InterPro; IPR001007; WIFC.			
DR	pfam; PF00007; Cys_knot; 1.			
DR	pfam; PF00050; lsp_1; 1.			
DR	pfam; PF00053; wvc; 1.			
DR	pfam; PF00019; IGFBP; 1.			
DR	SMART; SM0041; CT; 1.			
DR	PSM0222; IGF_BINDING; 1.			
PROSITE; PS01185; CTCK; 1; 1.				
PROSITE; PS01225; CTCK_2; 1.				
DR	PS01228; WIFC; 1.			
KW	Cell adhesion; DNA synthesis; Extracellular matrix; Signal.			
FT	SIGNAL	1		

Query Match Best Local Similarity 44.3%; Score 937; DB 1; Length 349; Matches 172; Conservative 61; Mismatches 100; Indels 38; Gaps 8;

Query 10 ALVVVLLHLTRLA-TCPAACHGCLP-EAPKCAPGVLGVLRDGGCCRVCAKOLNE-DSKT 67

Db	12 AFVLLALCSRPASSQDCSAPCCPAGPAPRCPAGSVLVDGGCCRVCAKOLNE-DSKT 71
QY	68 QPDHTKGLECNAGASSTALKGICRAGSEGRGECEYNSRIYQESTOPNCKHQCTDGA 127
Db	72 DEDPHKGICPDGSPANKRKIGVAT-DGAP-VEGGTVYQGESFQSCKTQCTG 130
QY	128 VGCIPLCQELSLPNLGGPNPRUVKGQCCEDSIKDPMEQDGKLGKELGFD 187
Db	131 VGCVPPLCSVDFVRPLSPDCPFPKPKGKCEEWVCDB---PKHEH--WVGPA 179
QY	188 SEVELTRNNELAVKGSSLKLRLPVFGMNEPRIYLNQLQGKCIWOTWSWSQSKTCGTG 247
Db	180 -----AAYRPDTFGDPTMI---RANLVQTEWSACKTGTG 217
QY	248 STRVNDNPCEREVKEVICEVPGQRYSSKKRKSCKRKSPERVRFYAGCLSV 307
Db	218 STRVNDNAFCREKOSLICMRPCADELEENKKGKICRPPKSKPIKEFLSGTSMK 277
QY	308 KYRPKYCSCVQDRCCTPQLTREVKMRFRCEGETESKNVMMIQLSQCKNYCPHANEAAF 367
Db	278 TYRAFKCGVCTDGRCTPHRTTLPVEFKCPDGEVMKKSMMPFIKTCACHYNGCPGDNDIFE 337
QY	368 PFT-RLFNDI 376
Db	338 SLVYKMYGDM 348

RESULT 7

ID	CYCF_PIG	STANDARD;	PRT;	349 AA.
AC	O19113;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Connective tissue growth factor precursor.			
GN	CYCF.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TAXID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Uterus;			
RX	MEDLINE-97390475; PubMed-9242708;			
RA	Brigitstock D.R., Steffen C.L., Kim G.Y., Vegunta R.K., Diehl J.R., Hardin P.A.;			
RT	"Purification and characterization of novel heparin-binding growth factors in uterine secretory fluids. Identification as heparin-			

RESULT 10
NOV_HUMAN STANDARD; PRT; 357 AA.
ID NOV_HUMAN STANDARD; PRT; 357 AA.
AC P4845; Q96BY5;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NOV protein homolog precursor (NovH) (Nephroblastoma overexpressed gene protein).
GN NOV.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94336229; PubMed=7520150;
RA Martinelli C., Huff V., Joubert T., Badzioch M., Saunders G.F., Strong L.C., Perbal B.;
RT "Structural analysis of the human nov proto-oncogene and expression in Wilms tumor.";
RL Oncogene 9:2739-2742(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strauberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ/GenBank databases.
CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: INCREASED EXPRESSION IN WILMS TUMOR OF THE STROMAL TYPE.
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 VMPC DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
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CC
DR EMBL; X78351; CAA55146.1;
DR EMBL; X78352; CAA55146.1; JOINED.
DR EMBL; X78353; CAA55146.1; JOINED.
DR EMBL; X78354; CAA55146.1; JOINED.
DR EMBL; X96584; CAA65403.1; -.
DR EMBL; BC015028; AAH15028.1; -.
DR Genew; HGNC:7885; NOV.
DR MIM; 164938; -.
DR InterPro; IPR000359; CYS_knot.
DR InterPro; IPR00067; Insl_gro_fac_pr.
DR InterPro; IPR000884; TSPL.
DR InterPro; IPR00107; WFP_C.
DR Pfam; PF00007; Cys_knot_1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; wmc_1.
DR Pfam; PF0021; IGFBP_1.
DR SMART; SM00041; CT_1.
DR SMART; SM00121; IB_1.
DR SMART; SM00209; TSP_1.
DR SMART; SM00214; WMC_1.
DR PROSITE; PS00222; IGR_BINDING_1.
DR PROSITE; PS0185; CPCK_1; 1.
DR PROSITE; PS01245; CRCK_2; 1.
DR PROSITE; PS01208; WFP_C; 1.
DR proto-oncogene, Growth factor binding; signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 357 NOV PROTEIN HOMOLOG.

RESULT 11
NOV_XENLA STANDARD; PRT; 343 AA.
ID NOV_XENLA STANDARD; PRT; 343 AA.
AC P51609;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NOV protein homolog precursor (Xnov).
GN NOV.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257227; PubMed=8666280;
RA Ying Z., King M.L.;
RT "Isolation and characterization of xnov, a Xenopus laevis ortholog of the chicken nov gene.";
RL Gene 171:243-248 (1996).
CC -!- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 VMPC DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.

FT CARBOHYD 91 91, N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARRHYD 277 277, N-LINKED (GLCNAC. . .) (POTENTIAL).
 SEQUENCE 354 AA; 38928 MW; 08EC8C9C67829DB CRC64;

Query Match 38.9%; Score 823; DB 1; Length 354;
 Best Local Similarity 44.2%; Pred. No. 2.6e-54;
 Matches 161; Conservative 48; Mismatches 119; Indels 36; Gaps 9;

QY 7 RALALVWTLH-LTRALIS-TCPAAC-HCPLAEPKCAPGVGLVRCCGCKVKCAQLINE 62
 8 RCLCTLGFLPHLHSQVASLRCPSPRCPKPSISPCTCPGYSVLSQGCSCCPVCANQRE 67

QY 63 DCSKTKOPCDHKTGLENGFAGSASTALKGICRAQESEGCPCEYNSRITYONGESTQPNCHEQCT 122
 68 SCSEMARPDCDOSGLICDRSADPNQNTGICMV-PEGDNCFEDGVIRRNGEKFEPNCOYFCI 126

QY 123 CIDGAGVGCILCPQESLSPNPGCPNPRLVKVTGOCCEEWYCEDS1KDPMEDQDGIGKE 182
 127 CRDGGCGCPLRCQDLYDILPGPDCPABRPAVKAQVPGCEKEWKTCGSDE---QGTGIG-G 180

QY 183 LGFDASEVELTRNNEELAVKGKSSLKRLPVFGMPEPRILYNPLQGOKCIVOTTWSQSKT 242
 181 LALPAYRPEAVGVVE---SDSSI-----NCIEQSTEWMSCSKS 216

QY 243 CGTGISTRVTDNPPECRLVETRICVRPCQQ-PVYSSLKKGKCCSKTKEPEPVRTYA 301
 217 CGMGVSTRVTRNRRQCEMVKOTRCLCVRPCEPEEVTDKKKKCCLRTKSKLAIHQFE 276

QY 302 GCLSYTKYKPYRGCGSYDGRCTPOTLTTRVNMERGEDGEFSKNMMIQSCCKCNANCPh 361
 277 NCTSYTKPFCGCVSDGRCTPWNKTTQEVQDQLGETIKKPPVIGTCYSCNPQ 336

QY 362 ANEA 365
 QY 337 NNEA 340

RESULT 13
 BAR_3_CHTE STANDARD; PRT; 1700 AA.
 ID BAR_3_CHTE
 AC 003376;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Balbiani ring protein 3 precursor.
 BR3.
 OS Chironomus tentans (Midge).
 OC Eukaryota; Metazoa; Arthropoda; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoparia; Endopterygota; Diptera; Nematocera;
 OC Chironomoidea; Chironomidae; Chironominae; Chironomus.
 RN NCBL_TaxID=7153;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=90172404; PubMed=1689777;
 RT "Paulson G., Lendahl U., Galli J.J., Ericsson C., Wieslander L.; The Balbiani ring 3 gene in Chironomus tentans has a diverged repetitive structure split by many introns.";
 RL J. Mol. Biol. 211:331-349(1990).
 CC - FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR STRUCTURE, THE LARVAL TUBE. BABBIANI RING PROTEIN 3 COULD PLAY A ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS INTACELLULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THESE FORM FORMING WATER-INSOLUBLE FIBERS TOO EARLY.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - TISSUE SPECIFICITY: SALIVARY GLAND.
 CC - DOMAIN: HAS 82 APPROXIMATE REPEATS OF CYS-X-CYS-X-CYS.

RESULT 14
 MC1L_RAT STANDARD; PRT; 837 AA.
 ID MC1L_RAT
 AC P98089;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Intestinal mucin-like protein (MLP) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBL_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=92184794; PubMed=1371999;
 RA Xu G., Ruan L.-J., Khatri I., Wang D., Bennick A., Fahim R.E.F., Forstner G.G., Forstner J.F.;
 RT "CDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide";
 RL J. Biol. Chem. 267:5401-5407(1992).
 CC !- SUBCELLULAR LOCATION: Secreted.

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SO	SEQUENCE	379 AA:	41687 MW:	62BF0BBAAC5AFDE9 CRC64;	FT	CHAIN	25	379	CYR61;
SQ	SEQUENCE	379 AA:	41728 MW:	D2ABAED77B84762B CRC64;	FT	CHAIN	25	379	CYR61;
Query Match	91.6%	Score 193B;	DB 11;	Length 379;	Query Match	91.6%	Score 1937;	DB 11;	Length 379;
Best Local Similarity	91.4%	Pred. No. 4.2e-178;			Best Local Similarity	91.1%	Pred. No. 5.3e-178;		
Matches	350;	Conservative	9;	Mismatches	18;	Indels	6;	Gaps	2;
QY	1 MSSRIARALAVVTLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	QY	1 MSSRIARALAVVTLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	QY	1 MSSRIARALAVVTLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	QY	1 MSSRIARALAVVTLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	QY	1 MSSRIARALAVVTLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60
Db	1 MSSSTIKLAVAVTLLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	Db	1 MSSSTIKLAVAVTLLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	Db	1 MSSSTIKLAVAVTLLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	Db	1 MSSSTIKLAVAVTLLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60	Db	1 MSSSTIKLAVAVTLLHLTRALASTCPAHCLEAPKCAPGYGLVRDGGCKVKACQL 60
QY	61 NEDCSKTQPCDHKGLECNFGASSTALKGICRAQSEGRPECEYNSRITQNGESFQPNCHQ 120	QY	61 NEDCSKTQPCDHKGLECNFGASSTALKGICRAQSEGRPECEYNSRITQNGESFQPNCHQ 120	QY	61 NEDCSKTQPCDHKGLECNFGASSTALKGICRAQSEGRPECEYNSRITQNGESFQPNCHQ 120	QY	61 NEDCSKTQPCDHKGLECNFGASSTALKGICRAQSEGRPECEYNSRITQNGESFQPNCHQ 120	QY	61 NEDCSKTQPCDHKGLECNFGASSTALKGICRAQSEGRPECEYNSRITQNGESFQPNCHQ 120
Db	121 CTCIDGAVGCIPQOELSLPNCPRFLVKVSGQCCEWYCDEDISKDQDPL- 178	Db	121 CTCIDGAVGCIPQOELSLPNCPRFLVKVSGQCCEWYCDEDISKDQDPL- 178	Db	121 CTCIDGAVGCIPQOELSLPNCPRFLVKVSGQCCEWYCDEDISKDQDPL- 178	Db	121 CTCIDGAVGCIPQOELSLPNCPRFLVKVSGQCCEWYCDEDISKDQDPL- 178	Db	121 CTCIDGAVGCIPQOELSLPNCPRFLVKVSGQCCEWYCDEDISKDQDPL- 178
QY	181 KELGFDAEVELTRNELLAVKGSSLKRLPVFGMERICILYPL- OGOKCIVQTWSQ 238	QY	181 KELGFDAEVELTRNELLAVKGSSLKRLPVFGMERICILYPL- OGOKCIVQTWSQ 238	QY	181 KELGFDAEVELTRNELLAVKGSSLKRLPVFGMERICILYPL- OGOKCIVQTWSQ 238	QY	181 KELGFDAEVELTRNELLAVKGSSLKRLPVFGMERICILYPL- OGOKCIVQTWSQ 238	QY	181 KELGFDAEVELTRNELLAVKGSSLKRLPVFGMERICILYPL- OGOKCIVQTWSQ 238
Db	179 -LGFDASAEVLTTRNELLATKGSSLKRLPVFGTEPRVLPNUHAGOKCIVQTWSQ 236	Db	179 -LGFDASAEVLTTRNELLATKGSSLKRLPVFGTEPRVLPNUHAGOKCIVQTWSQ 236	Db	179 -LGFDASAEVLTTRNELLATKGSSLKRLPVFGTEPRVLPNUHAGOKCIVQTWSQ 236	Db	179 -LGFDASAEVLTTRNELLATKGSSLKRLPVFGTEPRVLPNUHAGOKCIVQTWSQ 236	Db	179 -LGFDASAEVLTTRNELLATKGSSLKRLPVFGTEPRVLPNUHAGOKCIVQTWSQ 236
QY	239 CSKRGTCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 298	QY	239 CSKRGTCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 298	QY	239 CSKRGTCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 298	QY	239 CSKRGTCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 298	QY	239 CSKRGTCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 298
Db	237 CSKSGTGCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 296	Db	237 CSKSGTGCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 296	Db	237 CSKSGTGCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 296	Db	237 CSKSGTGCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 296	Db	237 CSKSGTGCGISTRVTNDNPCECRVKETRICEVRCGQPVYSSLLKKKCSKTKSPEVRF 296
QY	299 TYAGCLSKYRKYKCYGSCVDGRCTPOLTRVKMRFRCEGEDGETFSKVNMMIQSCCKNYN 358	QY	299 TYAGCLSKYRKYKCYGSCVDGRCTPOLTRVKMRFRCEGEDGETFSKVNMMIQSCCKNYN 358	QY	299 TYAGCLSKYRKYKCYGSCVDGRCTPOLTRVKMRFRCEGEDGETFSKVNMMIQSCCKNYN 358	QY	299 TYAGCLSKYRKYKCYGSCVDGRCTPOLTRVKMRFRCEGEDGETFSKVNMMIQSCCKNYN 358	QY	299 TYAGCLSKYRKYKCYGSCVDGRCTPOLTRVKMRFRCEGEDGETFSKVNMMIQSCCKNYN 358
Db	297 TYAGCSYRKYKCYGSCCVGDRCCTPLQTRVKMRFRCEGEDGMFSKVNMMIQSCCKNYN 356	Db	297 TYAGCSYRKYKCYGSCCVGDRCCTPLQTRVKMRFRCEGEDGMFSKVNMMIQSCCKNYN 356	Db	297 TYAGCSYRKYKCYGSCCVGDRCCTPLQTRVKMRFRCEGEDGMFSKVNMMIQSCCKNYN 356	Db	297 TYAGCSYRKYKCYGSCCVGDRCCTPLQTRVKMRFRCEGEDGMFSKVNMMIQSCCKNYN 356	Db	297 TYAGCSYRKYKCYGSCCVGDRCCTPLQTRVKMRFRCEGEDGMFSKVNMMIQSCCKNYN 356
QY	359 CPHANEAAFPYRLFDIHKFRD 381	QY	359 CPHANEAAFPYRLFDIHKFRD 381	QY	359 CPHANEAAFPYRLFDIHKFRD 381	QY	359 CPHANEAAFPYRLFDIHKFRD 381	QY	359 CPHANEAAFPYRLFDIHKFRD 381
Db	357 CPHNEASERFLYSLFNDIHKFRD 379	Db	357 CPHNEASERFLYSLFNDIHKFRD 379	Db	357 CPHNEASERFLYSLFNDIHKFRD 379	Db	357 CPHNEASERFLYSLFNDIHKFRD 379	Db	357 CPHNEASERFLYSLFNDIHKFRD 379
RESULT 2									
QWTTMG	PRELIMINARY;	PRT;	379 AA.						
AC	QWTTMG9;								
DT	01-NOV-1999 (TREMBLREL. 12; Created)								
DT	01-NOV-1999 (TREMBLREL. 12; Last sequence update)								
DT	01-JUN-2002 (TREMBLREL. 21; Last annotation update)								
DE	CIR61 precursor.								
GN	CIR61.								
OS	Rattus norvegicus (Rat).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.								
OX	NCBI_TAXID=10116;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=IM; TISSUE=AORTA;								
RA	Unoki H., Yonekura H., Furukawa K., Yamamoto H.;								
RT	*Rat CIR61 mRNA.*								
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.								
DR	EMBL; AB015877; BA78339.1; -.								
DR	InterPro; IPR000599; Cys knot.								
DR	InterPro; IPR00867; insl_gro_fac_pr.								
DR	InterPro; IPR00884; TSP1.								
DR	InterPro; IPR00107; WFE_C.								
DR	Pfam; PF00007; Cys_knot; 1.								
DR	Pfam; PF0219; IGFBP; 1.								
DR	Pfam; PF00090; tsp_1; 1.								
DR	Pfam; PF00093; vwc; 1.								
DR	SMART; SM00041; CT; 1.								
DR	SMART; SM00121; IB; 1.								
DR	SMART; SM00209; TSP1; 1.								
DR	SMART; SM00214; VWC; 1.								
DR	PROSITE; PS01185; CTCK_1; 1.								
DR	PROSITE; PS01225; CTCK_2; 1.								
DR	PROSITE; PS0022; IGF_BINDING; 1.								
DR	PROSITE; PS01208; WFEC; 1.								
KW	Signal.								
FF	SIGNAL	1	24	POTENTIAL.					

QY	366	AFPFY--RLFLNDI	376	Db	271	VKTYRAKFCGCGTGDRCPTPHRTATLPVEFKCPDGEMIKRKMMFIKTCACHYNCPGDNDI	330	Db	169	-EOTRVGPALLAVRQEETYGPDSSIMR-----ANCLVQTTEWSACSK	209				
Db	331	FESLYFRRMYGM	343	Db	210	TCGNGISTRVTDNEMCRLEQKQLSCMVRPCAEALEENKKGKICRITKISKVPEFLS	269	Db	242	TCCGIGISTRVTDNAPCRLVKETRICEVRPGQQPVYSSLKKKKCSKTKSPVERFTYA	301				
Db	330	GCUSVKKYRPKCGSCCVDPGCCBOLTRAKMRPRCEDGETFSKVNMMIQSKCNYNCPH	361	Db	270	GCTSVKTRAKFCGVCTDGRCPTPHRTATLPVEFKCPDGEMIKRKMMFIKTCACHYNCPG	329	Db	362	ANEAFPY--RLNDI	376				
QY	330	DNDIFESMYRMKGDM	346	Db	330	DNDIFESMYRMKGDM	346	Db	330	DNDIFESMYRMKGDM	346				
RESULT 10				RESULT 11				RESULT 11							
OPPB0	PRELIMINARY;	PRT;	347 AA.	OPPB0	PRELIMINARY;	PRT;	349 AA.	OPPB0	PRELIMINARY;	PRT;	349 AA.				
ID	09780;			ID	097765			ID	097765						
AC				AC				AC							
DT	01-MAY-2000	(TREMBREL.	13, Created)	DT	01-MAY-1999	(TREMBREL.	10, Created)	DT	01-MAY-1999	(TREMBREL.	10, Last sequence update)				
DT	01-JUN-2002	(TREMBREL.	21, Last annotation update)	DT	01-JUN-2002	(TREMBREL.	21, Last annotation update)	DT	01-JUN-2002	(TREMBREL.	21, Last annotation update)				
DE	Connective tissue growth factor.			DE	Connective tissue growth factor.			DE	Connective tissue growth factor.						
GN	CTGF			GN	CIRF			GN	CIRF						
OS	Nothophthalmus viridescens (Eastern newt) (<i>Triturus viridescens</i>)			OS	Sus scrofa (Pig).			OS	Sus scrofa (Pig).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;			OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;			OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus;						
OC	Nothophthalmus.			OC	NCBI_TaxID:9823;			OC	NCBI_TaxID:9823;						
OX	NCBI_TaxID:8316;			OX	[1]			OX	[1]						
RN	[12]			RN	SEQUENCE FROM N.A.			RN	SEQUENCE FROM N.A.						
RP				RP				RP							
RC	TISSUE=FORELIMB BLASTEMA;			RC	TISSUE=UTERUS;			RC	TISSUE=UTERUS;						
RX	"MEDLINE-99033008; PubMed=9813273;			RX	Harding P.A.; Brinstock D.R.;			RX	Harding P.A.; Brinstock D.R.;						
RA	Cash D.E., Gates P.B., Tomkawa Y., Brookes J.P.;			RA	"Cloning and sequencing of a porcine connective tissue growth factor			RA	"Cloning and sequencing of a porcine connective tissue growth factor						
RT	"Identification of newt connective tissue growth factor as a target of			RT	(CIGF) cDNA.;			RT	(CIGF) cDNA.;						
RT	retinoic acid regulation in limb blastemal cells.";			RT	Submitted (SIRP-1998) to the EMBL/GenBank/DBJ databases.			RT	Submitted (SIRP-1998) to the EMBL/GenBank/DBJ databases.						
RL	Gene 22:119-114(1998); EMBL; AJ271167; CAB65965.1; -.			RL	EMBL; U70050; AAC00174.1; -.			RL	EMBL; U70050; AAC00174.1; -.						
DR	InterPro; IPR000359; Cys_knot.			DR	InterPro; IPR000359; Cys_knot.			DR	InterPro; IPR000359; Cys_knot.						
DR	InterPro; IPR000867; Insl_gro_fac_pr.			DR	InterPro; IPR000867; Tsp1.			DR	InterPro; IPR000867; Tsp1.						
DR	InterPro; IPR00884; Tsp1.			DR	InterPro; IPR00884; Tsp1.			DR	InterPro; IPR00884; Tsp1.						
DR	InterPro; IPR001007; VWFC_C.			DR	InterPro; IPR001007; VWFC_C.			DR	InterPro; IPR001007; VWFC_C.						
DR	Pfam; PF00007; Cys_knot; 1.			DR	Pfam; PF00007; Cys_knot; 1.			DR	Pfam; PF00007; Cys_knot; 1.						
DR	Pfam; PF00219; IGFBP; 1.			DR	Pfam; PF00219; IGFBP; 1.			DR	Pfam; PF00219; IGFBP; 1.						
DR	Pfam; PF00090; tsp1; 1.			DR	Pfam; PF00090; tsp1; 1.			DR	Pfam; PF00090; tsp1; 1.						
DR	Pfam; PWMC; 1.			DR	Pfam; PWMC; 1.			DR	Pfam; PWMC; 1.						
DR	SMART; SM00041; CT; 1.			DR	SMART; SM00041; CT; 1.			DR	SMART; SM00041; CT; 1.						
DR	SMART; SM00121; IB; 1.			DR	SMART; SM00121; IB; 1.			DR	SMART; SM00121; IB; 1.						
DR	SMART; SM00209; TSP1; 1.			DR	SMART; SM00209; TSP1; 1.			DR	SMART; SM00209; TSP1; 1.						
DR	SMART; SM00214; VWFC; 1.			DR	SMART; SM00214; VWFC; 1.			DR	SMART; SM00214; VWFC; 1.						
DR	PROSITE; PS01185; CTCK_1; 1.			DR	PROSITE; PS01185; CTCK_1; 1.			DR	PROSITE; PS01185; CTCK_1; 1.						
DR	PROSITE; PS01225; CTCK_2; 1.			DR	PROSITE; PS01225; CTCK_2; 1.			DR	PROSITE; PS01225; CTCK_2; 1.						
DR	PROSITE; PS00222; IGF_BINDING; 1.			DR	PROSITE; PS00222; IGF_BINDING; 1.			DR	PROSITE; PS00222; IGF_BINDING; 1.						
DR	PROSITE; PS01208; VWFC; 1.			DR	PROSITE; PS01208; VWFC; 1.			DR	PROSITE; PS01208; VWFC; 1.						
DR	SEQUENCE	347 AA;	38098 MW;	DR	SEQUENCE	349 AA;	37946 MW;	DR	SEQUENCE	349 AA;	37946 MW;				
Query Match	43.5%	Score 920.5;	DB 13;	Query Match	41.7%	Score 882;	DB 6;	Query Match	41.7%	Score 882;	DB 6;				
Best Local Similarity	45.4%	Pred. No. 2,7e-01;	Length 347;	Best Local Similarity	43.5%	Pred. No. 1,3e-76;	Length 347;	Best Local Similarity	43.5%	Pred. No. 1,3e-76;	Length 347;				
Matches	171;	Conservative	48;	Matches	162;	Mismatches	59;	Matches	162;	Mismatches	59;				
QY	9	LALWVTLHLRLALTCPAACHCPEAKPAGPVGLWRDGGCCYCAKQNLNECDSKT	68	QY	10	ALWVTLHLRLALTCPAACHCPEAKPAGPVGLWRDGGCCYCAKQNLNECDSKT	67	QY	68	QCDHTKGLECNFGASSTALKGICRAOSEGRCEYNRSRYQESFPNCKHOCTCIGA	127				
QY	1	: : : : : : : : : : : : : :	69	QCDHTKGLECNFGASSTALKGICRAOSEGRCEYNRSRYQESFPNCKHOCTCIGA	127	QY	72	ACPDPHKSLGCFDRGSPANRKIGVYCTAK-DCAPCVFGGTWYRSSESFOSSCKYQCTCLDGA	130	QY	128	VGGIPLCPOELSLPNLGGPNPRLVKVTGOCCEEWNCDEDSIKPDMODGLLGKELGDA	187		
Db	12	LILAVALLSWSCA-ODCSGERCRCPPKRPCECPAGTSLVMDGCKVKCAKQNLNECDSKT	70	Db	12	AFFVLLALGCSRPSQGDGSGOCAGAKRRAACPAGVSSILEGGCCRLCAKHLDLCIER	71	Db	131	VGCVPLCSDMVRIPSDCPFPRVLPKPKCCEEWVCQDP	169	QY	188	SEVELTRNNELLAVGKSSLKLRL-PVFGMERILYPLQGOKCIVOTTWSOCSKTCCTG	246
Db	69	PCDHHTGLECNFGASSTALKGICRAOSEGRCEYNRSRYQESFPNCKHOCTCIGA	128	Db	72	ACDPDPHKSLGCFDRGSPANRKIGVYCTAK-DCAPCVFGGTWYRSSESFOSSCKYQCTCLDGA	130	Db	170	--KDHVVGPALAYRIEDTFEPDTAM----RANGLVQTEWSACKTCCTG	216	QY	189	EVELTRNNELLAVGKSSLKLRL-PVFGMERILYPLQGOKCIVOTTWSOCSKTCCTG	241
QY	71	VCDPHHGLFCDFGSRSRKKIGVYCTAK-DGATCPVFGGMVYRGESFOSSCKVQCTCLDGG	129	QY	129	GCIPLCPOELSLPNLGGPNPRLVKVTGOCCEEWNCDEDSIKPDMODGLLGKELGDA	188	QY	130	GCVPLCSDMVRIPSDCPFPRVLPKPKCCEEWVCQDP	168	QY	189	EVELTRNNELLAVGKSSLKLRL-PVFGMERILYPLQGOKCIVOTTWSOCSKTCCTG	241

QY	247	ISTRVTDNPECRUVKETRICEVRPGCGPVYSSILKKRKCSKTKSPBPVRYAGCLSV	306	Db	178	LALPAYRPREATVGVEL---SDSSI-----NCIQTTEWSACSKS	213
Db	217	ISTRVNDNASCRLEKOSRCKMVRPCAEADLEENIKKGKRKIRPKSKPVKFELSGCTSV	276	Qy	243	CGTGSTRTNDNPECRUVKETRICEVRPGCGQ-PVYSSILKKRKCSKTKSPBPVRYA	301
Qy	307	KYRKYCGSCVDRGCTPQLTVKMRCEGETFSKVMMAQSCKCNYNCPH	366	Db	214	CGMGLSTRVNRLQCEMVKOTRLCMVRPCEDGETFSKVMMAQSCKCNYNCPH	273
Db	277	KTYRAKRCVCTDGRCCTRPRHTTPVVEKCPDGEVMMKSMFIKTCACHYNCPGDNDF	336	Qy	302	GCLSVKK'RPKYCSCVDRGCTPQLTVKMRCEGETFSKVMMAQSCKCNYNCPH	361
Qy	367	FPPY-RLFENDI 376		Db	274	NCTSLYT'KPRFCGICSDGRCCTPFPNTKIQVERFOCLPQIITKKPVMWIGTCTCHSNCP	333
Db	337	ESYYRKWGD 348		Qy	362	ANEA 365	
RESULT 12							
08QZQ5		PRELIMINARY;	PRY;	351 AA.	09QZQ5		
ID	09QZQ5				ID	09388	
AC	09QZQ5:				AC	095388	
DT	01-MAY-2000	(TREMBlrel. 13, Created)			DT	01-MAY-1999	(TREMBlrel. 10, Created)
DT	01-MAY-2000	(TREMBlrel. 13, Last sequence update)			DT	01-MAY-1999	(TREMBlrel. 10, Last sequence update)
DE	NOV protein.				DE	01-JUN-2002	(TREMBlrel. 21, Last annotation update)
GN	NOV.				GN	Connective tissue growth factor related protein WISP-1.	
OS	Rattus norvegicus (Rat).				OS	WISP1.	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				OC	Homo sapiens (Human).	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus..				OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
RN	[1]				OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
RP	SEQUENCE FROM N.A.				OX	NCBI_TAXID=9606;	
RC	SPAIN-SPRAGUE-DAWLLEY;				RN	[1]	
RX	MEDLINE=20035752; PubMed=10570975;				RP	SEQUENCE FROM N.A.	
RA	Liu C., Liu X.J., Crowe P.D., Kelner G.S., Fan J., Barry G., Manu F.,				RC	TISSUE=ADULT LUNG, AND FETAL KIDNEY;	
RA	Lang N., De Souza E.B., Matz R.A.;				RX	MEDLINE=99061933; PubMed=984555;	
RT	"Nephroblastoma overexpressed gene (NOV) codes for a growth factor				RA	Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,	
RT	that induces protein tyrosine phosphorylation."				RA	Brush J., Taneyhill L.A., Deuel B., Lew M., Watanabe C., Cohen R.L.,	
RL	Gene 238:471-478(1999).				RA	Meilham M.F., Finley G.G., Quirke P., Goddard A.D., Hillian K.J.,	
DR	EMBL: AF171936; AAA49371.1; -.				RA	Gurney A.L., Botstein D., Levine A.J.;	
DR	InterPro; IPR000359; Cys_knot.				RT	"WISP genes are members of the connective tissue growth factor family	
DR	InterPro; IPR000667; Insl1_gro_fac_pr.				RT	that are up-regulated in wnt-1-transformed cells and aberrantly	
DR	InterPro; IPR000884; TSP1.				RL	expressed in human colon tumors.	
DR	InterPro; IPR001007; VWFC.				DR	Proc. Natl. Acad. Sci. U.S.A. 95:14717-14722(1998).	
DR	InterPro; IPR00007; Cys_knot; 1.				RN	[2]	
DR	PFam; PR00219; IGFBP; 1.				RP	SEQUENCE FROM N.A.	
DR	PFam; PR00050; tsp_1; 1.				RA	Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,	
DR	PFam; PR00093; vwc; 1.				RA	Jonge R.D., Schilhabel M., Schattevoy R., Dette M., Menzel U.,	
DR	SMART; SM00041; CT; 1.				RA	Rosenthal A.;	
DR	SMART; SM00121; IB; 1.				RL	Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.	
DR	SMART; SM00209; TSP1; 1.				DR	EMBL; AF007719; AAC96321.1; -.	
DR	SMART; SM00214; VWC; 1.				DR	EMBL; AR192304; AAP2231.1; -.	
DR	PROSITE; PS01185; CTCK_1; 1.				DR	InterPro; IPR000359; Cys_knot.	
DR	PROSITE; PS01225; CTCK_2; 1.				DR	InterPro; IPR000867; Insl1_gro_fac_pr.	
DR	PROSITE; PS00222; IGF BINDING; 1.				DR	InterPro; IPR001007; VWFC.	
DR	PROSITE; PS01208; VWFC; UNKNOWN_1.				DR	InterPro; IPR00007; Cys_knot; 1.	
SQ	SEQUENCE 351 AA; 3509 MW; 02619707DE7C1BFB CRC64;				DR	PFam; PR00219; IGFBP; 1.	
Query Match							
QY	Best Local Similarity 38.7%; Score 819.5; DB 11; Length 351;				DR	PFam; PR00090; tsp_1; 1.	
Matches	158; Conservative 50; Mismatches 117; Indels 39; Gaps 8;				DR	PFam; PR00093; vwc; 1.	
QY	7 RALAVVTLVHLTRLALST--CPAAC-HCPLAEPKCAPGVGLVRDGCCCCYCAQLINE 62				DR	SMART; SM00041; CT; 1.	
	: : : : : : : : : :				DR	SMART; SM00121; IB; 1.	
Db	8 QCLCLGFLHLMLQVSATLRCPSRCPSPSPTCARGVRSVLDGSCSCCPVQARQRE 67				DR	SMART; SM00209; TSP1; 1.	
QY	63 DCSTKTPCQHTKGECNFCAASSTALKGTCRAQSRRPCYNSRIVONGSFQPKCKHQCT 122				DR	SMART; SM00214; VWC; 1.	
Db	63 SCSEMRPCQHQSSGLYCDRSPADPNNETGKMY-PRGDNCVFDGVYNGKFEPOQYCT 126				DR	PROSITE; PS01185; CTCK_1; 1.	
QY	123 CIDGAVGCPLCPOELSLNLGCNPRLVKVGTGCCCEWCDEDSIKDPMEDQGLGE 182				DR	PROSITE; PS01225; CTCK_2; 1.	
Db	127 CRDQGIGCVPQRQDVLGPDGDCAPKKAvgPGCCEKMG-----SEEGTIG-G 177				DR	PROSITE; PS01208; VWFC; UNKNOWN_1.	
QY	183 LGFDAEVEILTRNNBLIAVKGSSLKLRLVFGMPRTILNPLOCQKCIYOTTSMQSCT 242				SQ	SEQUENCE 367 AA; 40331 MW; 9F29CA94D69C0502 CRC64;	
Query Match							
QY	Best Local Similarity 38.3%; Score 771; DB 4; Length 367;				Matches	149; Conservative 61; Mismatches 125; Indels 54; Gaps 9;	
QY	2 SSRIARALAVHLTRLALST-----CPAAC-HCPLAEPKCAPGVGLVRDGCCCCYCAQLINE 54				DR	18 STVIALTSLAPTMDFPAPLEDSSRQFCWKCECPSPRCPPLGSLITGCECK 77	

QY 55 VCAKOLNEDCSKTPQDHTKGLECNF-GASSFLALKGICRASEGRCEYNSRIVONGESF 113
DR SMART; SM00121; IB; 1.
Db MCAQOLQGDNCTERAICDPHRGLYCDYSGRPRYIAIGVC-AQVVGVCVLGDGVRYNINGQSF 136
DR SMART; SM00203; TSP1; 1.
QY 114 QPNCKHOTCTCIDGAVGCIPCLPQELSPNLGPNPRLVKVQGQCBEWMCEDSIKPMF 173
DR PROSTB; PS01185; CTCK_1; 1.
Db 137 QPNCKHOTCTCIDGAVGCIPCLPQELSPNLGPNPRLVKVQGQCBEWMCEDSIKPMF 194
DR PROSTB; PS01225; CTCK_2; 1.
Db 174 DODGLICKELGEDA-SEVELTTRNNEILAVGKSSLKLRLPVFGMELPRILYNPLQGKCIWQ 232
DR PROSTB; PS01208; VWC; UNKNOWN_1.
Db 195 TAPRDIG--AFDAVGVEEANHR-----CIAV 219
DR PROSTB; PS01208; VWC; UNKNOWN_1.
QY 233 TTWSWSDCSKTCTGTSRVTNDNPPECRLVKETRICEVRPCGQPVSSIKGGKKCSKTKKS 292
DR TSPWSPGOSTSCGIGVSTRISNVNAQCWPESRCLNLRCPDVOIHTLIKAGKKLAVYQP 279
Db 293 PEPVRFYAGCLSVKVKRPKVCGSCVDGRCTPQLRTVKARFRCDEGETSKNMVIQS 352
DR 280 EASMFNTLAGCISTRSYOPKYCGVCMDFNRCCIPYKSTTDIVSFQCPDGLGFSSRQVLIWINA 339
QY 353 CKCNYNYPHANEAAPPFYRLNDIHKFRD 381
Db 340 GFCNLSCRNPND-----IFADLESYPD 361
DR 175 OPGLCKRELGKRELDAEVLTRNNEILAVGKSSLKLRLPVFGMELPRILYNPLQGKCIWQ 234
Db 194 QPALIDTRAFFAASGAAEQRYEN-----CIAV 221
ID 054775 PRELIMINARY; PRT; 367 AA.
AC 054775;
DT 01-JUN-1998 (T_{REMBL}rel. 06, Created)
DT 01-JUN-1998 (T_{REMBL}rel. 06, Last sequence update)
DT 01-JUN-2002 (T_{REMBL}rel. 21, Last annotation update)
DE ELM1.
GN ELM1 OR WISPL.
OS Mus musculus (mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEN;
RX MEDLINE=98119879; PubMed=9449709;
RA Hashimoto Y., Shindorokada N., Tani M., Nagamachi Y., Takeuchi K.,
RA Shiroishi T., Toma H., Yokota J.;
RT "Expression of the Elm1 gene, a novel gene of the CCN (connective tissue growth factor, CytR/Cef10, and neuroblastoma overexpressed gene) family, suppresses *in vivo* tumor growth and metastasis of K-1735 murine melanoma cells";
RT J. EXP. MED. 187:289-296(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY;
RX MEDLINE=99061933; PubMed=9843955;
RA Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,
RA Brush J., Taneyhill L.A., Dueel B., Lew M., Watanabe C., Cohen R.L.,
RA Melham M.F., Finley G.G., Quiske P., Goddard A.D., Hillian K.J.,
RA Gurney A.L., Botstein D., Levine A.J.;
RT "WISP genes are members of the connective tissue growth factor family that are up-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors.";
RT PROC. NATL. ACAD. SCI. U.S.A. 95:14717-14722(1998).
DR EMBL; AB004873; AAC06319.1;
DR EMBL; MG:1197008; WISPL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000867; insl_gro_fac_pr.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF00007; CYS_knot; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00121; IB; 1.

RESULT 14
ID 054775
AC 054775;
DT 01-JUN-1998 (T_{REMBL}rel. 06, Created)
DT 01-JUN-1998 (T_{REMBL}rel. 06, Last sequence update)
DT 01-JUN-2002 (T_{REMBL}rel. 21, Last annotation update)
DE ELM1.
GN ELM1 OR WISPL.
OS Mus musculus (mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HEN;
RX MEDLINE=98119879; PubMed=9449709;
RA Hashimoto Y., Shindorokada N., Tani M., Nagamachi Y., Takeuchi K.,
RA Shiroishi T., Toma H., Yokota J.;
RT "Expression of the Elm1 gene, a novel gene of the CCN (connective tissue growth factor, CytR/Cef10, and neuroblastoma overexpressed gene) family, suppresses *in vivo* tumor growth and metastasis of K-1735 murine melanoma cells";
RT J. EXP. MED. 187:289-296(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY;
RX MEDLINE=99061933; PubMed=9843955;
RA Pennica D., Swanson T.A., Welsh J.W., Roy M.A., Lawrence D.A., Lee J.,
RA Brush J., Taneyhill L.A., Dueel B., Lew M., Watanabe C., Cohen R.L.,
RA Melham M.F., Finley G.G., Quiske P., Goddard A.D., Hillian K.J.,
RA Gurney A.L., Botstein D., Levine A.J.;
RT "WISP genes are members of the connective tissue growth factor family that are up-regulated in wnt-1-transformed cells and aberrantly expressed in human colon tumors.";
RT PROC. NATL. ACAD. SCI. U.S.A. 95:14717-14722(1998).
DR EMBL; AB004873; AAC06319.1;
DR EMBL; MG:1197008; WISPL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000867; insl_gro_fac_pr.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF00007; CYS_knot; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00090; tsp_1; 1.
DR Pfam; PF00093; vwc; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00121; IB; 1.

RESULT 15
ID 099PP0
AC 099PP0;
DT 01-JUN-2001 (T_{REMBL}rel. 17, Created)
DT 01-JUN-2001 (T_{REMBL}rel. 17, Last sequence update)
DT 01-JUN-2002 (T_{REMBL}rel. 21, Last annotation update)
DE ELM1.
GN ELM1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY;
RX MEDLINE=20487548; PubMed=11031104;
RA Sleeman M.A., Hurison J.G., Strachan L., Kumble K.D., Glenn M.P.,
RA McGrath A., Bickerstaff P., Grierson A., Havukkala I., Tan P.,
RA Watson J.D.;
RT "Gene expression in rat dermal papilla cells: analysis of 2529 ESTs.";
RT Genomics 69:210-224(2000).
DR EMBL; AF228049; AAK0729.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR000867; insl_gro_fac_pr.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF00007; CYS_knot; 1.
DR Pfam; PF00219; IGFBP; 1.
DR Pfam; PF00090; tsp_1; 1.
DR SMART; SM00041; CT; 1.
DR SMART; SM00121; IB; 1.

DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS01165; CTRK_1; 1.
 DR PROSITE; PS01225; CTRK_2; 1.
 DR PROSITE; PS01208; VVFC; UNKNOWN 1.
 SQ SEQUENCE 367 AA; 40613 MW; 8A4A34C69D3243D2 CRC64;

 Query Match 35.9%; Score 759; DB 11; Length 367;
 Best Local Similarity 38.5%; Pred. No. 9. 6e-65; Gaps 8;
 Matches 149; Conservative 52; Mismatches 130; Indels 56;
 Matches 149; Conservative 52; Mismatches 130; Indels 56; Gaps 8;

 Qy 5 IARALALVVTIHLTRLALST-----CPAACHCPLAPKCAPGVGLVRDGCGCKVCA 57
 Db 21 LATALSPTPTMTFTRPLECTITRFECKWPKPCQAPPKPCPLGVSLLTGCECKICA 80

 Qy 58 KOLNEPCSKNQPCDHTRKGLECNF-GASSTALKGICRAOSECRPCEVNSRTYONGESFQPN 116
 Db 81 QQLGDNCTEAAVCDPHRGLYCDYSGDRPRRYAIGVC-AQVVGVGVCLDGVRYTINGESFQPN 139

 Qy 117 CKHQCTCIGAVGCPLIC--POELSLPNLGPNPRLYKVQVQCCSERWCEDDSIKPMED 174
 Db 140 CRYNCHCIDGSTVGCTPLCLSPRP--PRLMCROPRHVRVPQCCSEWWCDDARR--PR 193

 Qy 175 QDGLGKELGFDASEVELTRNNELIAVGKSSLKLRLPVFGMEPRILYNPLQGQKCTVQTT 234
 Db 194 QTALLTTRAFASAAGAVEQRVEN-----CIATS 221

 Qy 235 SWSOCRTCGNGISTRVNDNPECRVKEKTRICEVRPGQPVYSSLUKKGKKSCTRKSPE 294
 Db 222 PWSPCSTTCGLGISTRISNVNRCWPQECSRULCNLRPCDVDIRPHIKAGKKCLAVYQPEE 281

 Qy 295 PVRFTYAGCULSVKVKYRKPGSCVDRCTQLTTRVMMRRCEDGETFSKNMMSIQCK 354
 Db 282 ATNFETLAGCVSTRTRYAPKCYGVCTDNRCCTIPSKTISVDFQCPGEPEGSFQVWLWINACF 341

 Qy 355 CNYNCNHAEEAPPYRLFNDIHKFRD 381
 Db 342 CNLSCRNPND-----IFADESYPD 361

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 Job time : 83 secs

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